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March 13, 2006, 18:52:59; Search time 75.2941 Seconds (without alignments) 58.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 TVSGNILTIR 10
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SUMMARIES

Score Ma 47 10	h Length 0 0 10	8 7 8	ID AAY05980	Descrip
70	100.0 10	7	AAY05988	Aav059
10	0.00	4	AAE07788	Aae0778
2	.00.0	4	AAE07728	AAA0773
10	100.0 15	4	AAE07726	AAP0773
10	0.00	4	AAE07727	72000V

Description		Aav05980 Human can	Human	Human			_	Human	Human	Human	Human	Human	_			_	-	_		Adi19048 Human HLA	Peptid	Adz67819 Major his		HI.A-DE	_	
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AAE07717	AAU85110	ABG79131	ADG89697	ADQ10452	ADS80932	ADK68648	ADK68657	ADQ10455	ADS80935	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818
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27	30	36	54	123	123	179	179	179	179	180	180	180	180	180	180	180	180	180	180	180
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lolon cancer; metastasis; melanoma; adentocarcinoma; thymoma; colon cancer; uterine cancer; breadt cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127. AAY05980 standard; peptide; 10 AA. (first entry) 16-AUG-1999 AAY05980; RESULT 1

Homo sapiens. WO9918206-A2. vaccine.

(USSH) US DEPT HEALTH & HUMAN SERVICES. Rosenberg SA; WPI; 1999-277270/23. Wang RF,

97US-0061428P. 98WO-US019609,

21-SEP-1998; 08-OCT-1997;

15-APR-1999.

Claim 17; Page 64; 88pp; English. Cancer antigen NY ESO1/CAG-3.

This sequence represents cancer peptide ESO10-127 that corresponds to amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAV5596), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAV5966), portions of them and their against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of

prostate, ovarian, pancreatic and thyroid cancers

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cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HiA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer, and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                          100.0%; Score 47; DB 2; Length 10; 100.0%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                            return to a patient
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                   Sequence 10 AA;
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leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
                                                                                                     NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
                                                                                Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 42; 88pp; English.
                    AAY05988 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                            Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                          97US-0061428P
                                                                                                                                                                                                                                                       98WO-US019609
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                    Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                         WPI; 1999-277270/23
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                       21-SEP-1998;
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                                                                                                                                                                                                              WO9918206-A2
                                                             16-AUG-1999
                                                                                                                                                                                                                                  15-APR-1999
                                         AAY05988;
                                                                                                                                                                                                                                                                                                                    Wang RF,
RESULT 2
           AAY05988
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This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see AAXS8S99). 30 Epitopes (see AAYOS988-Y06017) were identified. The present peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1 ORF1 (see AAXOS965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAXOS967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lampoma, lamp cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
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Sequence 14 AA;

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1 The MHC-II epitopes from the cancer antigen, NY ESO-1 and human leucocyte from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC: epitope; cancer antigen; NY ESO-1 protein; CD4 T lymphocyte; human leuccoyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                            ö
                                                                                        Length 10;
                                                                                                                                         0; Indela
                                                                                          100.0%; Score 47; DB 2; 100.0%; Pred. No. 0.004;
                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      AAE07788 standard; peptide; 14 AA.
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29-SEP-2000; 2000US-0237107P.
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                                                                                                                                            Conservative
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                                                                                                                                                                                                1 TVSGNILTIR 10
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                                                                                                                    Local Similarity
les 10; Conserv
                                              Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAE07788;
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                                                                                                Query Match
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                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                          RESULT 3
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RESULT

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) darived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NV ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by aliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of calls expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or happen and to induce tumour-specific humoralment arget antigen and/or happen and to induce tumour-specific humoralment restricted T cell epitope of human NY ESO-1 protein
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                               Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                             ö
100.0%; Score 47; DB 4; Length 14; 100.0%; Pred. No. 0.0061; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Human NY ESO-1 MHC class II restricted T cell epitope #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                         AAE07728 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 16; 134pp; English.
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29-SEP-2000; 2000US-0237107P.
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                                                                                                                                                                                                                                                                                       (first entry)
                                       10; Conservative
                                                                           1 TVSGNILTIR 10
                                                                                                             TVSGNILTIR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenberg SA,
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                 Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                   AAE07728;
   Query Match
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                                                                                                                                                                       RESULT 4
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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitopes) darived from the cancer antigen, NY 850-1. The MHC-II epitopes (C from NY 850-1 are recognised by CD4 T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP creaticted. The products of the gene are promising candidates for HLA-DP creaticted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given the generation of happen and/or hapten and to induce tumour specific humoral-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mediated immunity against cancer. The present sequence is MHC class II restricted T cell epitope of human NY ESO-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                            Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope, MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                      Human NY ESO-1 MHC class II restricted T cell epitope #12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                   AAE07726 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 16; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-2001; 2001WO-US002765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protection from metastasis.
                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-496851/54.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 WO200155393-A2
                                                                                                                                                                                                                                                                  immunotherapy.
                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                06-NOV-2001
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                                                         AAE07726;
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AAE0772
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Gaps

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100.0%; Score 47; DB 4; Length 14; 100.0%; Pred. No. 0.0061; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100. Matches 10; Conservative

TVSGNILTIR 15

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us-09-529-206e-15.rag

Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.

(first entry)

06-NOV-2001

Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC:II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leuccoyte antigen; HLA; tumour-epecific humoral-mediated immunity; cancer; cytostatic;

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epicope (MHC-II epitope) derived from the cancer antigen, NV ESO-I. The MHC-II epitopes from W ESO-I are recognised by CD+T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD+T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+T cell responses against any given
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or
                                                                                                                                                                                                                                                                                                                                         Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
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                                                                                                                                                                                                                                                                 Human NY ESO-1 MHC class II restricted T cell epitope #13.
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                                       AAE07727 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 16; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001WO-US002765
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                                                                                                                                                                                              (first entry)
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-496851/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                              06-NOV-2001
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                                                                                                                   AAE07727;
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AABO7727

ID AABO

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Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                              100.0%; Score 47; DB 4; Length 15; 100.0%; Pred. No. 0.0067; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                AAE07787 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                 06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                      1 TVSGNILTIR 10
                                                                                                                                                                                                                                                    Local Similarity
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Gaps

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AAE07786 standard; peptide; 15 AA.

RESULT 7

AAE07786

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TVSGNILTIR

TVSGNILTIR 10

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The invention relates to the identification and isolation of major (histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitopes) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes crowing the cancer antigen, NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted anner, in particular HLA-DR or HLA-DR crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention. Leatment and diagnosis of patients with cancer. The cancer the recipient as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T clymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral.

CC peptide used in the characterisation of the NY ESO-1 epitope recognised by TE4-1

New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as

Example 6; Fig 6A; 134pp; English.

protection from metastasis.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P. 26-JAN-2001; 2001WO-US002765

WO200155393-A2.

02-AUG-2001

immunotherapy Homo sapiens ö

Rosenberg SA,

Wang R,

WPI; 2001-496851/54.

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The invention relates to the identification and isolation of major histocompatibility (MHG) class II restricted T cell epitope (MHG-II epitope) derived from the cancer antigen, NV ESO-I. The MHG-II epitopes from NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The preducts of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in amammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral mediated immunity against cancer. The present sequence is human NV ESO-I peptide used in the characterisation of the NV ESO-I epitope recognised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer; tumour; antigen; MHC; major histocompatility complex; Class II; T-cell; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoms; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4 T lymphocyte; human leuccoyte antigen; tumour-specific humoral-mediated immunity; cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumour antigen NY-ESO-1 peptide #13.
                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                         Zeng G;
                                                                                                                                                                                                                                             26-JAN-2001; 2001WO-US002765.
                                                                                                                                                                                                                                                                                      28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protection from metastasis.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Rosenberg SA,
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                                                                                                                                                             WO200155393-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
                                                                                immunotherapy
                                                                                                                           Homo sapiens
                                                                                                                                                                                                       02-AUG-2001
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tumour antigen, NY-ESO-1 (AAYS2430) which can bind to MHC(major historiality Class II HIA-DRS3 molecules, thereby stimulating proliferation of helper T-cells. GNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer CDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal covary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and preast encer, specimens, ovariant and encer, thyroid cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells
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HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                                                                                                  Old LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 47; DB 3; Length 18; 100.0%; Pred. No. 0.0084; ... o. Mismatches 0; Indels
                                                                                                                                                                                                                                    Alexander K,
                                                                                                                                                                                                                                  Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NY-ESO-1 HLA-DR53 binding motif #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69940 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 22; 49pp; English.
                                                                                                                                                                                                                                  Chen Y,
                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                     98US-00165546.
                                                                                                                       99WO-US006875.
                                                                                                                                                      98US-00062422
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                                                                                                                                                                                                                                                                                  WPI; 2000-038483/03.
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Gure A, Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
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                             Homo sapiens,
                                                           WO9953938-A1
                                                                                                                        24-MAR-1999;
                                                                                                                                                      17-APR-1998;
                                                                                                                                                                       02-OCT-1998;
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                                                                                         28-OCT-1999
              Synthetic.
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14-JUL-2000; 2000WO-US019220

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05-APR-2001.
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                                                                                                                                                                                                                     The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small
                                                                                                                                  Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
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                                                                                     Scanlan M;
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                     Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                   Old LJ, Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NY-ESO-1 HLA-DR53 binding motif #6.
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                                                                                                                                                                                                                                                                                                                                                 lung carcinoma or bladder carcinoma
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                                                CANCER RES
                                                                                                                                                                                               Example 16; Page 27; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69944 standard; peptide; 18 AA.
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                                  LUDW-) LUDWIG INST CANCER RES
                                               SLOK ) SLOAN KETTERING INST C
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(CORR ) CORNELL RES FOUND INC.
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            99US-00359503
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Best Local Similarity 100.
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                                                                                   Stockert E,
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                                                                                                            WPI; 2001-182822/18
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
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            23-JUL-1999;
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                                                                                   Jager E,
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                                                                                                                                                                          patient.
                                                                                                                                   Method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; muman leukocyte antigen-determining region; disease progression; disease carefresion; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a human NY-ESO-1 tumour rejection antigen precursor fragment which recognises and binds to HIA-DRE3. WY-ESO-1 and SGX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MRC) class II molecules such as human leukocyte antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-DR53 recognising NY-ESO-1 peptide #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 19; 62pp; English.
                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01544 standard; peptide; 18 AA.
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                                                                                                                                           50pp;
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nes 10, Conservative
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                                                                                                                                      Example 16; Page 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-266156/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive bubject in order to stimulate the helper T cells. An MHC Class II HLA-DR. WY-BSO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunorsactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onest of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the
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Sequence 18 AA;

ö Gaps .; 0 100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084; tive 0; Mismatches 0; Indels 10; Conservative Local Similarity Query Match Matches

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AAU01540 standard; peptide; 18 AA. RESULT 13

(first entry) 18-JUL-2001 AAU01540;

HLA-DR53 recognising NY-ESO-1 peptide #2.

NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; human leukocyte antigen-determining region; disease progression; disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.

Homo sapiens.

WO200123560-A2

05-APR-2001

26-SEP-2000; 2000WO-US026411.

99US-00408036 29-SEP-1999; (LUDW-) LUDWIG INST CANCER RES.

Pfreundschuh M;

Sahin U,

Tureci O,

WPI; 2001-266156/27.

leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells. Polypeptides binding to major histocompatibility complex class II human

Example 13; Page 19; 62pp; English.

precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigendetermining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in sequence represents a human NY-ESO-1 tumour rejection antigen

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free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoractive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the
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88888888888888888

Sequence 18 AA;

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Gaps
                                ö
100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084; ive 0; Mismatches 0; Indels
                                10; Conservative
                Local Similarity
 Query Match
                                Matches
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ö

ò 셤 RESULT

AAE07769

AAE07769 standard; peptide; 18 AA.

AAE07769;

(first entry) 06-NOV-2001 Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope, MHC-II epitope, cancer antigen; WH SSO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy

Homo sapiens.

WO200155393-A2.

02-AUG-2001.

26-JAN-2001; 2001WO-US002765.

28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang R, Rosenberg SA,

WPI; 2001-496851/54.

New NY-ESO cancer peptide or MHC class II restricted ${\tt T}$ cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

Claim 84; Page 84; 134pp; English.

The invention relates to the identification and isolation of major histocompatibility (MIC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NV ESO-I. The MHC-II epitopes from NV ESO-I are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of partients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-I gene product. The cancer peptides are also

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The invention describes an isolated NY-ESO-1 peptide (I), consisting of amino acids 80-109, 87-98, 108-119, 121-132 or 143-154 of a sequence of 180 (S1) amino acids fully defined in the specification. Also described are: a composition (II) useful in stimulating a CD4 + T cell response, comprising (I) and an adjuvant; a composition (III) useful in stimulating a T cell response in a subject, comprising (I) and at least one additional peptide; an isolated nucleic acid molecule (IV) consisting of a nucleotide sequence which encodes a peptide, where the amino acid sequence is chosen from 80-109, 87-98, 108-119, 121-132 or 143-154 of 180 of (S1); an expression vector (V) comprising (IV) operably linked to a promotex; a recombinant cell (VI) comprising (IV) a recombinant cell (VII) comprising (IV) and an isolated CD4 + T cell (VIII) which crecognizes a complex of (I) and a major histocompatibility complex (MHC) class II molecule. (I) is useful for treating cancer. This is the amino acid acid sequence of a NY-ESO-1 peptide.
                                                                                                                                                                                                ö
useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 HIA DR restricted T cell cancer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; immune stimulation; cancer; cytostatic; neoplasm; NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel NY-ESO-1 peptide that binds to human leukocyte antigen class II molecules, useful for treating cancer.
                                                                                                                                                                                                Gaps
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                                                                                                                                                      100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.0084;
                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                               ADW50855 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2003; 2003US-0474893P
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                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2005 (first entry)
                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NY-ESO-1 peptide 121-138
                                                                                                                                                                                                                                                          7 TVSGNILTIR 16
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                                                                                                                   Sequence 18 AA;
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0; Gaps

Query Match 100.0%; Score 47; DB 9; Length 18; Best Local Similarity 100.0%; Pred. No. 0.0084; Matches 10; Conservative 0; Mismatches 0; Indels

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Qy 1 TVSGNILTIR 10
| | | | | | | | | |
Db 7 TVSGNILTIR 16
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Search completed: March 13, 2006, 19:03:56 Job time: 77.2941 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-15

1 TVSGNILTIR 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	major tail protein	lipoic Acid Synthe		hypothetical prote	ribosomal protein	translation initia	2-hydroxyacid dehy	hypothetical prote		hetical	н	R prote	MATE efflux family	hypothetical prote		N-acetylglutamate	probable amino-aci	serotonin receptor	serotonin receptor	serotonin receptor	5-hydroxytryptamin	serotonin receptor	hypothetical prote			hypothetical prote		conserved hypothet	5-HT2c receptor -
ΩI	T13099	AD2753	B97534	A89837	RSBSOF	T41234	AB3218	G86835	A85989	F91143	TPBPP1	S18683	G95241	B98106	F85253	B81033	A81977	802011	A43956	S11280	S40689	A34863	E96674	T02759	F71405	C86898	B81972	D81029	137105
80	~	7	7	7	Н	7	~	~	7	~	-	~	7	~	~	~	7	7	~	~	7	~	N	~	~	~	~	~	7
% Query Match Length	245	323	323	335	177	244	311	314	1266	1266	144	144	411	426	428	436	436	449	471	471	471	471	876	918	1996	102	121	135	187
% Query Match	76.6	9.9/	9.9/	74.5	72.3	72.3	72.3	72.3	72.3		70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2		70.2	70.2	70.2		70.2	70.2	68.1	68.1	68.1	68.1
Score	36	36	36	35	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32
Result No.	-	7	Э	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	probable oxidoredu	Iysozyme (EC 3.2.1	hypothetical prote	conserved domain p	conserved hypothet	uncharacterized pr	S-adenosylhomocyst	hypothetical prote	sigma 1 protein pr	serotonin receptor	serotonin receptor	serotonin receptor	serotonin receptor	alkylhalidase ĥomo	
H75390	S57550	C87158	S25234	A69325	G95146	E98014	C97059	E70401	865162	HMXRS3	JS0616	A43951	A32605	S23562	T30590	ALIGNMENTS
N	~	~	N	~	N	N	N	~	~	Н	N	N	~	~	7	
234	245	289	316	344	347	347	376	418	451	455	458	459	460	479	491	
68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	68.1	
32	32	32	32	32	32	35	32	32	32	32	32	32	32	32	32	

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A;Accession: T13099
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-245 <HEN>
A;Cross-references: UNIPROT:O64327; UNIPARC:UPI000009BA91; EMBL:AF064539; NID:g3192683; C;Genetics:
                                                             C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13099 #
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
submitted to the EMBL Data Library, May 1998
A;Reference number: 217603
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                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2;
Pred. No. 14;
1; Mismatches
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C;Superfamily: phage lambda major tail protein V
                                                                                                                                                                                                                                                                                                                                                                                         76.6%;
77.8%;
                    major tail protein V - phage N15 N; Alternate names: protein gpl3
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 77.8
les 7; Conservative
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T13099
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lipoic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AD2753
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 'serage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel, Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Accession: AD2753
A,Accession: AD2753
A,Status: preliminary

A,Molecule type: DNA A,Residues: 1-323 -KKUR> A,ECTOSS-references: UNIPROT:QBUFG1, UNIPARC:UPIO00012E6BE; GB:AE008688; PIDN:AAL42442.1 A,Experimental source: strain C58 (Dupont)

C'Genetics: A/Gene: lipA A/Agp position: circular chrom C,Superfamily: lipoyl synthase

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ribosomal protein L6 - Bacillus stearothermophilus
N.Alternate names: ribosomal protein BL10
C;Species: Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 0.2-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A02766; B39085; S59061
R;Kimura, M.; Rawlings, N.; Appelt, K.
FEBS Lett. 136, 58-64, 1981
A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the Bacillus st
A;Reference number: A02766
A;Accession: A02766
A;Accession: A02766
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A; Residues: 1-177 < KIM>
A; Residues: 1-177 < KIM>
A; Residues: 10.177 < KIM>
A; Cross-references: UNIPARC: UNIPARC: UPI0000050F95
B; Ramakrishnan, V.; Gerchman, S.E.
J. Biol. Chem. 266, 880-885, 1991
A; Electrope: Cloning; sequencing, and overexpression of genes for ribosomal proteins from Ba A; Reference number: A39085; MUID:91093287; PMID:1985969
A; Accession: B39085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-244 <LYN>
A;Residues: 1-244 <LYN>
A;Cross-references: UNIPROT:094476; UNIPARC:UPI000012D3B6; EMBL:AL035075; PIDN:CAA22640
A;Cross-references: uniprot: 972h-; cosmid c1919
C;Genetics:
A;Gene: SPDB:SPCC1919.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 8-170 cRAM>
A; Cross-references: UNIPPARC:UP10000173A98; GB:M57622
A; Cross-references: UNIPPARC:UP10000173A98; GB:M57622
B; Urlaub, H.; Kruft, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A; Title: Protein-rRNA binding features and their structural and functional implications
A; Reference number: S59051; MUID:96003638; PMID:7556101
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24;
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A,Molecule type: DNA
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Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: ribosomal protein L6/L9
C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 149-163 <URL>
A;Cross-references: UNIPARC:UP10000173A99
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55.6%;
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75.0%;
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TVEGNVITV 51
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141 TVAGNVLT 148
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Best Local Similarity
Matches 6; Conserv
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A; Introns: 12/2; 36/2
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: A89837
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Tinoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Recession: A89837
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-335 AKUR>
A; Cross-references: UNIPROT:Q99VV7; UNIPARC:UP100000549A2; GB:BA000018; PID:g13700555; F
A; Experimental source: strain N315
C; Genetics:
A; Gene: SA0619
C; Superfamily: probable sodium-dependent phosphate transporter MTH1885
                                                                                                                                                                                                                                                                                 lipoic acid synthetase (lip-syn) (lipoate synthase) [imported] - Agrobacterium tumefacie C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004 C;Accession: B97534
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: B97534
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 2, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: B97534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Crose-references: UNIPROT:Q8UFG1; UNIPARC:UPI000012E6BE; GB:AE007869; PIDN:AAK87227.1;
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                                                  DB 2; Length 323
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Pred. No. 30;
1; Mismatches
                                            Score 36; DB 2
Pred. No. 18;
1; Mismatches
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A/Gene: AGR C 2646
C/Superfamily: lipoyl synthase
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ilarity 70.0%;
Conservative 1
                                                  76.6%;
70.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                         Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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189 TVPGNYLTVR 198
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189 TVPGNYLTVR 198
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hypothetical protein EC84118 [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Escherichia coli (5.5pecies: B-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: F91143 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1266 <HAY>
A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI000000082E; GB:BA000007; PIDN:BAB37541.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Species: phage P1
C;Species: phage P1
C;Species: phage P1
C;Species: 19-28-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession. 353460
R;Guidolin, A.; Zingg, J.M.; Arber, W.
A;Fitle: Organization of the bacteriophage P1 tail-fibre operon.
A;Reference number: PS0109; MUID:89326122; PMID:2526777
A;Recession: JS0460
A;Molecule type: DNA
A;Residues: 1-144 <GUI>A;Residues: 1-144 <GUI>C;Genetics:
                A;Molecule type: DNA
A;Residues: 1-1266 <STO>
A;Residues: 1-1266 <STO>
A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI0000D082E; GB:AE005174; NID:g12517869;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4604
C;Superfamily: Escherichia coli hypothetical protein yhdp
                                                                                                                                                                                                                                                                    Score 34; DB 2; Length 1266;
Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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C;Superfamily: Bscherichia coli hypothetical protein yhdP
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C;Superfamily: phage Pl tail fiber protein R
C;Keywords: tail fiber
                                                                                                                                                                                                                                                                          72.3%;
66.7%;
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Best Local Similarity 66.79
Matches 6, Conservative
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Matches 6; Conservative
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1017 TISGNTLTL 1025
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79 TYSGGIITVR
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A;Status: preliminary
A;Molecule type: DNA
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2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens ('Species: Agrobacterium tumefaciens ('Species: Agrobacterium tumefaciens ('Space: 11-Jan-2002 #text_change 05-Oct-2004 C;Accession: AB318 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Kwood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dypothetical protein yreB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Accession: G8635 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: G8635 A;Accession: G8635 A;Cross-references: UNIPROT:Q9CEZ4; UNIPARC:UP1000000449D; GB:AE005176; PID:g12724702; FA;Cross-references: UNIPROT:Q9CEZ4; UNIPARC:UP1000000449D; GB:AE005176; PID:g12724702; FA;Genetics: A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: UNIPROT.Q8UJK3; UNIPARC:UP10000167CD3; GB:AE008687; PIDN:AAL46160.1;
A.Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                           ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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77.8%; Pred. No. 44;
tive 1; Mismatches
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C;Superfamily: 2-hydroxyacid dehydrogenase
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93 ISGNILTL 100
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Best Local Similarity
Matches 6; Conserv
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A,Molecule type: DNA
A,Residues: 1-311 <KUR>
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: 695241
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95241
A;Roccus references: UNIPROT:Q97NG5; UNIPARC:UPI000051ADC; GB:AE005672; PIDN:AAK76128.1;
A;Coss-references: UNIPROT:Q97NG5; UNIPARC:UPI000051ADC; GB:AE005672; PIDN:AAK76128.1;
A;Genetics:
A;Genetics:
gener R protein - Escherichia coli plasmid p15B
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 18689
R;Sandmeier, H.; Idad, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.
N;Title: Gene organization in the multiple DNA inversion region Min of plasmid p15B of E
A;Reference number: S18680; MUID:92051368; PMID:1945872
A;Reference number: SNA
A;Residues: translation not shown
A;Residues: 1-144 <SAN>
A;Residues: 1-144 <SAN>
A;Cross-references: UNIPROT:Q47426; UNIPARC:UP100000B4972; EMBL:X62121; NID:g42224; PIDN
A;Cross-references: UNIPROT:Q47426; UNIPARC:UP10000B4972; EMBL:X62121; NID:g42224; PIDN
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Pred. No. 31;
2; Mismatches
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A,Genome: plasmid
C,Superfamily: phage P1 tail fiber protein R
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Best Local Similarity 60.07
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A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98106
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-426 <KUR>
A;Residues: 1-426 <KUR>
A;Cross-references: UNIPROT:Q8DN77; UNIPARC:UPI00000E3724; GB:AE007317; PIDN:AAL00679.1
C;Genetics:
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C.Bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C.Accession: F85253
R.anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 769-777, 1999
A.Aitle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Reference number: A85001; MUID:20083488; PMID:10617198
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Modecule type: DNA
A,Residues: 1-428 <STO>
A,Cross-references: UNIPROT:Q9SUG4; UNIPARC:UPI00000A1769; GB:NC_001268; NID:g7269062; i
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Pred. No. 98;
3; Mismatches
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C,Superfamily: F-box containing protein
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL, AF038567; AAD05202.1; -; mRNA.
HGNC; HGNC: 2491; CTAGIB.
MIM; 300156; -.
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDIJINE=99289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen B., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
                              05x554
05zvd1
05zvd1
05lnu4
05lea1
09pt82
09irp9
06irp9
06irp9
06irp9
08t4d0
09ve00
09ve00
              QSWWD6_LEGPL
QSXVD1_LEGPH
TOLB_STLPO
GSILEA1 BACFN
Q9PT83_XENLA
Q9PT83_XENLA
Q6NX22_XENTR
Q6NX22_XENTR
Q6NX22_XENTR
Q6NX22_DROME
Q9VSQ0_DROME
Q9VSQ0_DROME
Q9DRGQ_DROME
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NCBI_TaxID=9606;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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MEDLINE-21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
Nelson D.L.;
                                                                                                      100.0%; Score 47; DB 1; Length 180; 100.0%; Pred. No. 0.55;
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Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
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                                        Gly-rich.; B122C5C2C8BE1569 CRC64;
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                                                                                                                                                   0; Mismatches
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Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo sapiens (Human).
                      Potential.
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17992 MW;
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Q7LBY4;
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Best Local Similarity 100...
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Antigen; Transmembrane
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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-!- SIMILARITY: Belongs to the small heat shock protein (HSP20) family.
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100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.55;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
NON TER 1
SEQÜENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AP006840; BAD39931.1; -; Genomic_DNA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006986; P:response to unfolded protein; IEA.
InterPro; IRR002068; HBP20.
PROSITE; PS01031; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
Complete Proteome; Heat shock.
SEQUENCE 141 AA; 15725 WW; C7BABABCFC50FD36 CRC64;
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STRAIN=T / IAM 14863;
PubMed=15383646; DOI=10.1093/nar/gkh830;
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01-0CT-2000 (TrEMBLrel. 15, Last sequenc)
01-0CT-2002 (TrEMBLrel. 22, Last annotat
Hypothetical protein LAGE-2 (Fragment).
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25-OCT-2004 (TrEMBLrel. 28, Last
HSp20 family heat shock protein.
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80.0%;
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Q9NY13;
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Q67QW2;
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67 TVDGNMLTIR 76
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Query Match
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Theileria annulata.
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STRAINECE3;

MEDLINE-97286510; PubMed-9141657; DOI=10.1016/S0378-1097(97)00069-4;

Tate R., Riccio A., Iaccarino M., Patriarca E.J.;

"Cloning and transcriptional analysis of the lipA (lipoic acid
synthetase) gene from Rhizobium etli.";

FEMS Microbiol. Lett. 149:165-172(1997)

-!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
atoms into an octanoyl group bound to acyl carrier protein (ACP)

to produce a lipoyl group (By similarity).

-!- CATALYTIC ACTIVITY: octanoyl- [acyl-carrier protein] + 2 sulfurs =
                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last sequence update)
Lipoyl synthase (EC 2.8.1. -) (Lipoic acid synthase) (Lipoate synthase)
(Lipoyl acyl-carrier protein synthase) (Sulfur insertion protein lipA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               lipoyl-[acyl carrier protein]
-!-CORACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and an exchangeable S-adennosyl-L-methionine (By similarity).
-!-COFACTOR: Binds 1 3Fe-4S cluster (Potential).
-!-PATHWAY: Liboate biosynthesis; sulfur-insertion step.
-!-STMILARITY: Belongs to the biotin and lipoic acid synthetases
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (3Fe-4S) (Potential). (3Fe-4S) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
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Iron-sulfur 1 (3Fe-4S) (Potential)
Iron-sulfur 1 (3Fe-4S) (Potential)
Iron-sulfur 2 (4Fe-4S-S-AdoMet) (B
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InterPro; IPR006638; Elp3/Miab/NifB.

InterPro; IPR001698; Lipoate synth.

InterPro; IPR007199; Lipoate synth.

InterPro; IPR007199; Lipoate synth; 1.

PANTHER; PTHR10949; Lipoate synth; 1.

PIRSF; PTRSP005963; Lipoyl_synth; 1.

SMART; SM07729; Elp3; 1.

ITGRPAMS; TGR00510; lipA; 1.

ITGRPAMS; TGR00510; lipA; 1.

IFGRPAMS; AFe-4S; Iron; Iron-sulfur; Metal-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iron-sulfur 2 (4Fe-4S-S-AdoMet)
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
   2; Length 142;
                           Indels
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0
 Score 39; DB 2
Pred. No. 17;
1; Mismatches
                                                                                                                                         322 AA.
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                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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 83.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family. LipA subfamily.
                          8; Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                               Rhizobiaceae, Rhizobium, NCBI_TaxID=29449;
                                                                  101 TVSGNILTM 109
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                                                  1 TVSGNILTI 9
Query Match
Best Local Similarity
Matches 8; Conserv
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72
87
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                                                                                                                                                   005941;
15-JUL-1998
                                                                                                                                          RHIET
                                                                                                                                                                                                                                              Name=lipA;
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Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
Etienne J., Glaser P., Buchrisesr C.;
"Evidence in the Legionella pneumophila genome for exploitation of
host cell functions and high genome plasticity.";
Nat. Genet. 36:1165-1173(2004).
EMBL; CR628336; CAH12569.1; -; Genomic_DNA.
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Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrell B.G.;
"The chromosome I sequence of Theileria annulata.";
Submitted (APR-2005) to the ENBL/GenBank/DbBJ databases.
EMBL; CR940347; CA173760.1; - Genomic DNA.
SEQUENCE 617 As, 67272 MW; 2A3696230D209B70 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=lpp1418;
Legionella pneumophila (strain Paris).
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
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Pred. No. 63;
2; Mismatches 0; Indels
  Score 38; DB 1; Length 322;
Pred. No. 61;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37270 MW; 9BCB4B74CD8BB383 CRC64;
                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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13.5EF-2005 (TrEMBLrel. 31, Last sequence update)
13.5EF-2005 (TrEMBLrel. 31, Last annotation update)
Theileria parva Tpr-related protein, putative.
ORFNames=TA21390;
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CG) GO:005066; F:FAD binding; IEA.
GO; GO:0016491; F:Oxidoreductase activity; IEA.
GO; GO:0006491; F:Oxidoreductase activity; IEA.
GO:00000313; P:ENNA processing; IEA.
InterPro; IPR001269; Du Synth.
PROSITE; PS01136; UPP0034; 1.
COMPLETE PROCESSING; BYPOTHER PROSITE; PS01136; UPP0034; 1.
COMPLETE PROCESSING; DAS; 37270 MW; 9ECB4B74CD8BB383
                                                                                                                                                                                                                                                                                                       330 AA.
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  80.9%;
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77.8%;
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Q4UGM9;
Query Match 80.9
Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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188 TVAGNYLTVR 197
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204 TINGNILTI 212
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NUCLEOTIDE SEQUENCE
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us-09-529-206e-15.rup

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Query Match
Best Local Similarity
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PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
Ogata H., Renesto P., Audic Z., Robert C., Blanc G., Fournier P.-E., Parinello H., Claverie J.-M., Raoult D.;
The genome sequence of Rickettsia felis identifies the first putative conjugative plasmid in an obligate intracellular parasite.";
PLOS Biol. 3:E248-E248(2005).
EMBL; CP000053; AAY61019.1; -; Genomic_DNA.
InterPro; IRR007466; DUF497.
Pfam; PF04565; DUF497.
SEQUENCE 94 AA; 11378 MW; DG2F3CIDE3CF686E CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
BMBL, AE014295, AAN24266.1; -; Genomic_DNA.
GO, GO:0003824; F:catalytic_activity; IEA.
GO, GO:0009236; P:cobalamin biosynthesis; IEA.
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MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.,
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Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
14)-SEP-2005 (TrEMBLrel. 31, Last annotation update)
15-SEP-2005 (TrEMBLrel. 31, Last annotation update)
17-SEP-2005 (TrEMBLrel. 31, Last annotation update)
17-SEP-2005 (TrEMBLrel. 31, Last annotation update)
18-SEP-2005 (TrEMBLrel. 31, Last ann
                                          Score 38; DB 2; Length 617;
Pred. No. 1.2e+02;
2; Mismatches 1; Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                          2; Mismatches
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OrderedLocusNames=BL0429;
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                                              80.9%;
Ouery Match
Best Local Similarity 70.0.
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Q4UN39;
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Matches 7; Conservative
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451 TISGNTLTIK 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PUMPG=12F67720; DOI=10.1038/ng1447;

Pubmed=12F67720; DOI=10.1038/ng1447;

A richit M., Jarrand S., Brueggemann H., Zidane N., Magnier A., Ma L.,

Tichit M., Jarrand S., Bouchier C., Vandenesch F., Kunst F.,

Etienne J., Glaser P., Buchrisesr C.;

Etienne J., Glaser P., Buchrisesr C.;

Thost cell functions and high genome plasticity.";

Nat Genet. 36:1165-1173(2004).

It host cell functions and high genome plasticity.";

Nat Genet. 36:1165-1173(2004).

EBBL; CR628337; CAH15806.1; -; Genomic_DNA.

LegioList; Ipl1566; -. Genomic_DNA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0008033; P:tRNA processing; IEA.

RIFEPPO: IRROBLESG; Du_Synth.
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25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
26-007-2004 (TrEMBLrel 28, Last annotation update)
27-007-2004 (TrEMBLrel 28, Last annotation update)
28-007-2004 (TrEMBLrel 28, Last annotation update)
29-007-2004 (TrEMBL
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Legionella pneumobahila (grrain Lens).
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=297245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=272624;
                                                                                                                                                                                                                       Length 250;
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PROSTIE; PS01136; UPF0034; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 330 AA; 37311 MW; BEF935DAP152E15E CRC64;
                                                                                                                                   250 AA; 27653 MW; 7577954A609689CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            78.7%; Score 37; DB 2;
87.5%; Pred. No. 75;
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66.7%; Pred. No. 1e+02;
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PubMed=15448271; DOI=10.1126/science.1099776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA.
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                                                                                                                                                                                                                                                                                                                 1; Mismatches
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InterPro; IPR011698; GATase_3.
Pfam; PF07685; GATase_3; 1.
Complete proceome.
SEQUENCE 250 AA; 27653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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QSWW87 LEGPL PRELIMINARY;
OSWW87;
                                                                                                                                                                                  QSZVH8 LEGPH PRELIMINARY;
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21 SGNVLTIR 28
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064327 BPN15 PRELIMINARY;
064327;
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636 TIAGNILTV 644
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                       1 TVSGNILTI 9
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                                                                                                                                                                                                                                                                        N15-like viruses.
NCBI_TaxID=40631;
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                                                                                                                                                                                                                                Name=gene 13;
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064327 BPN15
ID 064327 PT
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Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M., Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J., Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R., Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., UIz M.E., Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G., Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J., The genomic sequence of the accidental pathogen Legionella
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"Annotation of the Genome of Candida albicans.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
"-I SUBGELLULAR LOCATION: Nuclear; nucleolar (By similarity).
EMBL; AACQ01000024; EALULS8.1; -; Genomic_DNA.
InterPro; IPR011989; ARN-1ike.
InterPro; IPR012978; DUF NUC173.
Feas; PF02985; HEAT.
Pfam; PF02161; NUC173.
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PubMed=15123810; DOI=10.1073/pnas.0401648101;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
"The diploid Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                         Length 334;
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SEOUENCE 1217 AA; 135897 MW; 1F2788D13CAD6DEC CRC64;
                                                                                                                                                      EMBL; AE017354; AAU27544.1; -; Genomic_DNA.
EMBL; AE0120165; F:PAD binding; IEA.
EQ; GO:0016491; F:exidoreductase activity; IEA.
EQ; GO:0016491; F:exidoreductase activity; IEA.
EMBL: PE0137; PHENA processing; IEA.
EMBL: PE0137; Dus; 1.
ENGSITE; PE0136; UPF0034; 1.
EMBL: PE0136; UPF0034; 1.
EMBL: PE0136; UPF0034; 1.
EMBL: PE0136; UPF0034; 1.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                      78.7%; Score 37; DB 2; 66.7%; Pred. No. 1e+02; tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSAFQ7_CANAL PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.7
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ORFNames=CaO19.7011;
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Best Local Similarity
Matches 6; Conserv
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Q5AFQ7 CAN
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STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
Read TD., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J., Duugherty S.C., DeBoy R.T., Dodgon R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanahevan J.J., Weidman J.F., Impraim M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Utterback T.R., McDonald L.A., Felablyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanila oneidensis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                      Bacteriophage N15.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V., Smirnov I.K.;
Smirnov I.K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF064539; AAC19050.1; -; Genomic_DNA.
PIR; T13099; T13099.
PIR; T13099; T13099.
PIR; F12099; T13099.
PRAMET; SM0635; B1Q_2:
SMART; SM06635; B1Q_2: 1.
SMART; SM06635; B1Q_2: 1.
SMART; SM06635; B1Q_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SO3842.
OrderedLocusNames=SO3842;
                                                                                                 Last sequence update)
Last annotation update)
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EMBL; AE015817; AAN56819:1; -; Genomic_DNA.
                                                                    Created)
PRT;
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                                                         01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-OCT-2003 (TrEMBLrel. 25,
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PIR; AD2753; AD2753

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last unotation update)
13-SEP-2005 (Rel. 48, Last unotation update)
14-SEP-2005 (Rel. 48, Last unotation update)
15-PEP-2005 (Rel. 48, Last unotation update)
(Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase)
(Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2323-2328(2001).

-!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur atoms into an octanoyl group bound to acyl carrier protein (ACP) to produce a lippyl group (By similarity).

-!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs = lippyl-[acyl-carrier protein].

-!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and an exchangeable S-adenosyl-L-methionine (By similarity).

-!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).

-!- ATMINAY: Lippoate biosynthesis; sulfur-insertion step.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- SUBCELLULAR EDORGATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=21608560; PubMed=11743193; DOI=10.1126/science.1066804;

MOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.F.,

Mond D.W., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).

MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Planagan C., Crowell C., Gurson J., Lomo C., Sar C., Strub G.,
Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Name-lipA; OrderedLocusNames-Atu1436, AGR C 2646;
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
                      76.6%; Score 36; DB 2; Length 318; 87.5%; Pred. No. 1.5e+02;
                                                                    0; Indels
                                                                                                                                                                                                                                                                   323 AA
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EMBL; AE008069; AAK87227.1; -; Genomic_DNA.
                                                                  1; Mismatches
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Query Match
Best Local Similarity 87.5.
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153 TVSGNIIT 160
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HAWAP; ME'00206; -; 1.

HAWAP; ME'00206; -; 1.

InterPro; IPR003698; Lipoate_synth.

InterPro; IPR00197; Radical_SAM.

PANTHER; PTHR10949; Lipoate_synth; 1.

PEANTHER; PTHR10949; Lipoate_synth; 1.

PIRSF; PTRSF005963; Lipoyl_synth; 1.

PIRSF; PTRSF005963; Lipoyl_synth; 1.

ITGRFAMS; TIGR00510; lipoyl_synth; 1.

ITGRFAMS; TIGR00510; lipoyl_topose; Iron; Iron-sulfur; Metal-binding;

Transferase.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                      Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 1 (3Fe-4S) (Potential).
Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By similarity).
                                                                                                                                                                                                                   Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
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                                                                                                                                                                                                                                       lron-sulfur 2 (4Fe-45-S-AdoMet)
similarity).
                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 323;
Pred. No. 1.5e+02;
.; Mismatches 2; Indels
                                                                                                                                                                                                                                                                  74B294773BC784D2 CRC64;
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Job time : 75.5882 secs
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LENGTH: 18 amino acids TYPE: amino acid
1009
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3379
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3471
4471
4711
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4711
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STATE: New York
COUNTRY: USA
US-09-359-503-9
Sequence 9, Appli
Sequence 8, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 125, Appli
Sequence 125, Appli
Sequence 126, Appli
Sequence 120, Appli
Sequence 7, Appli
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Sequence 58027, A
Sequence 42707, A
Sequence 2739, Ap
Sequence 329, App
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Sequence 13, Appl
                                                                 March 13, 2006, 19:14:49 ; Search time 18:5882 Seconds (without alignments) 44.477 Million cell updates/sec
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Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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-09-134-001C-5428
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US-09-270-767-58027
US-09-270-767-42707
US-10-104-047-2739
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US-09-344-040C-125
US-09-834-040C-125
US-09-834-040C-120
US-09-833-039A-120
US-08-791-495-7
US-08-791-829A-7
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US-09-408-036B-8
US-09-408-036B-12
US-09-191-495-9
US-08-937-263B-8
US-09-751-798-8
US-09-165-5460-15
US-09-145-5460-15
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                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                    572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Result

32, Appl 32, Appl 34, Appl 3247, Ap 325, Appl 25, Appl 25, Appl 25, Appl 25, Appl 11, Appl 11, Appl 7, Appl 8, Appl 8, Appl 8, Appl 8, Appl 11, Appl 7, Appl 8, Appl 8 5209, Sequence 32, Sequence 478 Sequence 478 Sequence 34, Sequence 25, Sequence 25, Sequence 25, Sequence 8, P. Sequence 11, Sequence 7, P. Sequence 8, P. Sequence 9, P. Sequenc Sequence Sequence Sequence US-09-341-461-35 US-09-341-461-35 US-08-134-200-5209 US-08-131-270-32 US-09-583-110-4783 US-09-583-110-4783 US-09-292-071-25 US-09-292-071-25 US-09-292-071-25 US-09-292-072-25 US-09-292-072-25 US-09-292-072-25 US-07-101-255-25 US-07-91-92-08 US-07-91-92-08 US-07-91-92-08 US-07-91-92-08 US-08-370-542-7 US-08-310-542-7 US-08-117-006-8

ALIGNMENTS

to MY

Sequence 9, Application US/09359503

Sequence 9. Application US/09359503

GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Anuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue ZIP: 10103 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage MCBLUM TYEE: DIBKECLE, 3.5 JULLI, 1737

COMEDUM TYEE: LIBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Worderfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503

FLILING DATE: Unly 23, 1999

CLASSIFICATION DATA:
APPLICATION NUMBER: 09/165,546

FILING DATE: October 2, 1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422

FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/052,422

FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

PRIOR APPLICATION NUMBER: US 08/752,182

FILING DATE: September 15, 1997

PRILING DATE: October 1996

ATTORNEY AGENT INFORMATION:
NAME: Hanson, NO. 6251603man D.
REFERENCE/DOCKET NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 752-5958

INFORMATION FOR SEQ ID NO: 9:
SEMEMBER: 10 and 10 and

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RESULT 3
US-09-165-546D-9
US-09-165-546D
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Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CT
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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REGISTRATION NUMBER: 30,946
REPERBNOE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 2; Length 18; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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APPLICATION NUMBER: US/09/165,546D FILING DATE: 02-0ct-1998
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/337,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGRYT INFORMATION:
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CORRESPONDENCE ADDRESS:
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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US-09-165-546D-13
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, alexander
TITLE OF INVENTION: Gethod for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: New York City
STATE: New York City
COUNTRY: USA
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                                                                                                                               100.0%; Score 47; DB 2; Length 18; 100.0%; Pred. No. 0.013;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                    0; Mismatches
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SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:

FILING DATE: July 23, 1999
CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422
FILING DATE: APPLICATION DATA:

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08 08/752,182
FILING DATE: 03-0ctober-1996
ATTORNEY/AGENT INFORMATION:

NAME: HARSON, NO. 6251603man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5466.1

TELECOMMUNICATION:

TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09359503 Patent No. 6251603
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TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-09-359-503-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-359-503-13
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Sequence 12, Application US/09408036B

Sequence 12, Application US/09408036B

Sequence 12, Application US/09408036B

GENERAL INFORMATION:

APPLICANT: Tureci, Ozlem

APPLICANT: Tahin, Ugur.

APPLICANT: Tahin, Ugur.

APPLICANT: Pfreundschuh, Michael

TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses

TITLE OF INVENTION UNMER: US/09/408,036B

CURRENT FILING DATE: 1999-09-29

PRIOR PPLICATION NUMBER: 09/144,040

PRIOR PILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 38

SEQ ID NO 12

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
    APPLICANT: Lucas, Sophie
; APPLICANT: Desmet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Godelaine, Daniele
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L0461/7005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617-720-2441
7 TVSGNILTIR 16
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wol
STREET: 600 At
CITY: Boston
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02210
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CURRENT APPLICATION NUMBER: US/09/408,036B
CURRENT APPLICATION NUMBER: 09/344,040
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 47; DB 2; Length 18; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 47; DB 2; Length 18; 100.0%; Pred. No. 0.013;
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                    COMPUTER: IBM
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 15, 1996
FILING DATE: October 15, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 6723832man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09408036B
Patent No. 6800730
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Salnin, Ugur
APPLICANT: Pfreundschuh, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
            STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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US-09-392-714-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth, Drijfhout, Jan W.
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STRET: Ge Fifth Avenue
CITY: New York City
STATE: New York
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COMPUTER READABLE FORM:

MEDIUM TYPE:

COMFUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT COCTOBER: 1997
REFERENCE/DOCKET NUMBER: 40,177
REFERENCE/DOCKET NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEPHONE: (212) 318-3000
TELEPAS. (212) 752-5958
INPORMATION POR SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
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US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08937263B
Patent No. 6274145
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Best Local Similarity 100.
Matches 10; Conservative
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 TVSGNILTIR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-937-263B-8
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Gaps
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APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, All O.
APPLICANT: Glue, All O.
APPLICANT: Glue, All O.
APPLICANT: Williamson, Barbara
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
FILE REPERENCE: LO461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER APPLICATION NUMBER: PCT/US98/14679
SARLIER APPLICATION NUMBER: PCT/US98/14679
SEALIER FEILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 25
LENGTH: 180
                                                                                                                                                                                                                                                                                                                             ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: 30,946
; REPERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPAX: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
SEQUENCE FOR SEQ ID NO: 8:
LENGTH: 10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 25, Application US/09392714A; Patent No. 6686147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 655517man D.
RECISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determi
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                         APPLICANT: Leth., Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
CURRENT GODELAINE, LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPERENCE: Lotail/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT APPLICATION NUMBER: PCT/US98/01445
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 125, Application US/09344040C
Partent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
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Best Local Similarity 100.00
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ORGANISM: Homo sapiens
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Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
COMPUTER: IBM
COPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIFICATION DATA:
                                                             100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 47; DB 2; Length 180; 100.0%; Pred. No. 0.16; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6723832man D. REGISTRATION NUMBERS: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-09-165-546D-15
                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 318-3000
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SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acid
TYPE: amino acid
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                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-392-714-25
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US-09-165-546D-15
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US-09-341-829A-9
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Patent No. 6673350

GRNERAL INFORMATION

APPLICANT: Sahin, Ugur

APPLICANT: Sahin, Ugur

APPLICANT: Pfreundschuh, Michael

TILE REFERENCE: LUD 5622.1

CURRENT APPLICATION NUMBER: US/09/833,039A

CURRENT APPLICATION NUMBER: US/09/833,039A

CURRENT APPLICATION NUMBER: US 09/409,455

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 
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100.0%; Pred. No. 4.6e+05;
tive 0; Mismatches 0; Indels
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FILE REFERENCE: LUD 5556.1

CURRENT APPLICATION NUMBER: US/09/344,040C

CURRENT FILING DATE: 1999-06-25

FRIOR APPLICATION NUMBER: US 09/105,839

PRIOR FILING DATE: 1998-06-26

PRIOR PILING DATE: 1998-06-26

FRIOR PILING DATE: 1997-05-05

FRIOR FILING DATE: 1997-05-05

LEWATH: 9

LEWATH: 9
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Best Local Similarity 100.
Matches 9; Conservative
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US-09-344-040C-125
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US-09-833-039A-125
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US-09-833-039A-125
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Search completed: March 13, 2006, 19:18:49 Job time: 18.5882 secs

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CURRENT APPLICATION NUMBER: US/10/182,506A
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Sequence 16, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 65, Appl
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Sequence 34, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 20, Appl
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                                                                                      March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds (without alignments) 69.096 Million cell updates/sec
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Sequence 3,
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Sequence 2
Sequence 8
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'Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
'Ggn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
'Ggn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
'Ggn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-182-506A-15

US-10-751-088-9

US-10-751-088-13

US-10-851-884-12

US-10-851-884-12

US-10-851-884-12

US-10-1851-884-12

US-10-1851-884-12

US-10-164-121A-35

US-10-164-121A-35

US-10-164-121A-35

US-10-164-121A-35

US-10-164-121A-35

US-10-182-506A-6

US-10-182-506A-6

US-10-296-734-1414

US-10-296-734-1414

US-10-296-734-1414

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US-10-296-734-1414

US-10-37-217-17
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US-10-207-655-71
US-10-026-066-3
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Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                US-09-529-206E-15
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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US-10-182-506A-15
Sequence 15, Application US/10182506A
Publication No. US20050136402A1
GENERAL INFORMATION:
APPLICANT: Wang, FF
APPLICANT: Resemberg, S A
TITLE OF INVENTION: NOVEL WHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
TITLE OF INVENTION: ANTIGEN, NY ESO-1
FILE REFERENCE: 217955
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15, Appl
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100.0%; Score 47; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels
US-10-117-937-74
US-10-295-027-386
US-10-296-027-386
US-10-188-832-139
US-10-777-053-11
US-10-777-053-11
US-10-877-217-11
US-10-877-217-11
US-10-877-217-11
US-10-877-217-11
US-10-875-023-30
US-10-871-708-7
US-10-875-523-3
US-10-182-506A-3
US-11-067-064-74
US-11-067-064-74
US-11-067-159-74
US-09-821-881-27
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic US-10-182-506A-17
      1 TVSGNILTIR 10
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APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.037; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                         ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION NUMBER: US/09/165,546D
FILING DATE: 02-OCC-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: APILI 17, 1998
APPLICATION NUMBER: 09/062,422
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/37,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: OCCODER: 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
       USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/10751088; Publication No. US20040158044A1
                                                                                                       STREET: 666 Fifth Avenue CITY: New York City STATE: New York
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OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
                                     NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
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GENERAL INCORPORTATION.

APPLICANT: Wang, R-F

APPLICANT: Rosenberg, S A

APPLICANT: Cang, G

TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER

TITLE OF INVENTION: ANTIGEN, NY ESO-1

FILE REFRENCE: 217955

CURRENT PAPLICATION NUMBER: US/10/182,506A

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: PCT/US01/02765

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR PRILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR PRILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.1

SEQ ID NO 16

LENGTH: 15

THENDEL TO NO 16

THENDEL TO NO 16

THENDEL TO NO 16

THENDEL TO NO 16
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Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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100.0%; Score 47; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 47; DB 5; Length 15; 100.0%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/USO1/02765
PRIOR FILING DATE: 2001-01-26
PRIOR PELICATION NUMBER: 60/179,004
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR PRIOR DATE: 2000-01-28
PRIOR PRIOR DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN VERSION 3:1
SEQ ID NO 15
LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 16, Application US/10182506A; Publication No. US20050136402A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10751088; Publication No. US20040158044A1
                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic US-10-182-506A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
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US-10-182-506A-16
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US-10-751-088-9
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WS-10-182-506A-65

Sequence 65, Application US/10182506A

Publication No. US20050136402A1

Sequence 65, Application US/10182506A

Publicant: Wang, R-F

APPLICANT: Wang, R-F

APPLICANT: Zeng, G

TITLE OF INVENTION: ANTIGEN, NY ESO-1

FILE REFERENCE: 217955

CURRENT APPLICATION NUMBER: US/10/182,506A

CURRENT FILING DATE: 2002-10-28

PRIOR PPLICATION NUMBER: 60/179,004

PRIOR PPLICATION NUMBER: 60/179,004

PRIOR PPLICATION NUMBER: 60/237,107

SOFTWARE: PatentIn version 3.1

SEQ ID NO 65

LENGTH: 18
                                                                      APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Ffreundschuh, Michael
TITLE NETENTRACE: LUD 5624
CURRENT APPLICATION NUMBER: US/10/851,884
CURRENT APPLICATION NUMBER: US/09/408,036
PRIOR APPLICATION NUMBER: US/09/408,036
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 47; DB 5; Length 18; 100.0%; Pred. No. 0.037; tive 0; Mismatches 0; Indels
           ; Sequence 12, Application US/10851884; Publication No. US20040214284A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic US-10-182-506A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-851-884-12
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Matches
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APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
TITLE ON TIVE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses OURRENT APPLICATION NUMBER: US/09/81,884
CURRENT APPLICATION NUMBER: US/09/408,036
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                        NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 antino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 47; DB 4; Length 18; 100.0%; Pred. No. 0.037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION S 30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORREY/AGRAT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-10-751-088-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10851884
Publication No. US20040214284A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-851-884-8
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RESULT 9 US-10-164-121A-35

RESULT

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GENERAL INFORMATION:

APPLICANT: VAN DER BRUGGEN, Pierre
APPLICANT: BOON-FALLEUR, Thierry
APPLICANT: BROCKPOT, Karine
APPLICANT: THIELBRANS, Kraine
APPLICANT: LUD-S83-US (10411307)
CURRENT FILING DATE: 2004-09-15
FILOR PAPLICATION NUMBER: US 60/504,874
PRIOR APPLICATION NUMBER: US 60/504,874
PRIOR FILING DATE: 2003-09-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.2
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US-10-941-150A-35
      PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/179,004
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/10941150A; Publication No. US20050226881A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic US-10-182-506A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 20
                                                                                                                                                                                                                                                     FEATURE:
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Sequence 35, Application US/10164121A
Publication No. US20030228308A1
GENERAL INPORMATION:
APPLICANT: Zhang, Yi
APPLICANT: Land, Thierry
APPLICANT: Traversari, Catra
APPLICANT: Traversari, Catra
TITLE OF INVENTION: 1801ated Peptides Which Bind to HLA-Cw6 Molecules And Uses ThereformERRENELLICATION WUMBER: US/10/164,121A
CURRENT APPLICATION UNMBER: US/10/164,121A
CURRENT FILING DATE: 2002-08-26
NUMBER: OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/10164078A
Publication No. US2030228325A1
GENERAL INFORMATION:
BAPPLICANT: Blaborough, Janine
APPLICANT: Schultz, Erwin
APPLICANT: Panichelli, Christophe
APPLICANT: Panichelli, Christophe
APPLICANT: Panichelli, Christophe
APPLICANT: Panichelli, Christophe
APPLICANT: Poon, Thierry
TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Therec
TITLE OF INVENTION: 1801ated Peptides Which Bind to HLA-B18 Molecules And Uses Therec
CURRENT APPLICATION UMBER: US/10/164,078A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 35
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Publication No. US20050136402A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosenberg, S A
APPLICANT: Zeng, G
TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER TITLE OF INVENTION: APPLICANT:
FILE REFERENCE: 217955
CURRENT FILLING NUMBER: US/10/182,506A
CURRENT FILLING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/02765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                     SEQ ID NO 35
LENGTH: 20
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Search completed: March 13, 2006, 20:02:26 Job time : 61.4706 secs
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; Sequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
    APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT FILING DATE: 2000-10-28
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR PLING DATE: 2000-01-28
; PRIOR PLING DATE: 2000-01-28
; PRIOR PLING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
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Publication No. US20050136402A1
GENERAL INFORMATION:
APPLICANT: Wang, R.F
APPLICANT: Rosenberg, S.A
APPLICANT: Zeng, G
TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
TITLE OF INVENTION: ANTIGEN, NY ESO-1
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CURRENT APPLICATION NUMBER: US/10/182,506A
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/02765
                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83
PRIOR APPLICATION NUMBER: FR01/13352
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.2
                                                                                      SEQ ID NO 83
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-182-506A-6
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Gaps
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PRIOR FILING DATE: 2001-01-26
PRIOR PLILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR APPLICATION DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 27
TYPE: PRI
                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Synthetic
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March 13, 2006, 19:54:06; Search time 6.82353 Seconds (without alignments) 40.793 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df				
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
7	47	100.0	20	-	US-11-032-498-36	Sequence 36, Appl
7	47	100.0	180	7	US-11-155-288-7	7, 1
٣	47	100.0	240	7	US-11-021-441-28	28
4	35	74.5	223	9	US-10-485-517-412	412,
₹2	34	72.3	305	7	US-11-098-686-10549	Sequence 10549, A
9	34	72.3	585	7	US-11-072-512-2739	Sequence 2739, Ap
7	33	70.2	313	7	US-11-190-188-7	
ω.	33	70.2	387	9	US-10-467-657-1556	Н
1,5	33	70.2	426	9	US-10-873-528-34	
10	33	70.2	471	9	US-10-995-561-901	901,
11	33	70.2	517	9	US-10-641-678-47	47, 7
12	32	68.1	105	9	US-10-485-788A-711	711,
13	32	68.1	105	7	US-11-053-076-81	81, A
14	32	68.1	123	9	US-10-467-657-1358	1358
15	32	68.1	523	9	US-10-641-678-45	45,
16	31	99	92	9	US-10-485-788A-657	Sequence 657, App
17	31	99	92	7	US-11-053-076-19	19,
18	31	0.99	536	9	US-10-641-678-70	70,
19	31	0.99	1085	7	US-11-087-099-11646	1164
20	31	0.99	2204	7	US-11-052-554A-174	Sequence 174, App
21	30	63.8	40	9	US-10-895-064-2370	Sequence 2370, Ap
22	30	63.8	40	7	US-11-129-741-2370	Sequence 2370, Ap
23	30	63.8	194	7	US-11-087-099-342	Sequence 342, App
24	30	63.8	201	ហ	US-09-810-501-21	Sequence 21, Appl
25	30	63.8	228	ഗ	US-09-978-360A-516	516

41, Appl 11290, A 43, Appl	3, 55, 159		54, A 5042, 232.	19, A 233, 1054,	2228, Ap 86, Appl 26866, A 6776, Ap	
Sequence	Sequence	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	22.22
US-10-511-538-41 US-11-098-686-11290 US-11-129-143-43	US-11-165-024-3 US-11-129-143-55 US-10-055-877-159	US-111-072-512-3928 US-111-087-099-390 US-111-124-368A-183	US-11-127-877-54 US-10-467-657-5042 US-11-052-554A-232	US-11-190-188-19 US-11-152-366-233 US-10-467-657-1054	US-10-467-657-2228 US-11-019-711-86 US-11-096-568A-26866 US-11-087-099-6776 US-11-124-368A-265	***************************************
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ALIGNMENTS

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Sequence 36, Application US/11032498
Sequence 36, Application US/11032498
Publication No. US20050249743A1
Publication No. US20050249743A1
SEQUENCE INFORMATION:
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Wan der Bruggen, Pierre
APPLICANT: Wan der Bruggen, Pierre
APPLICANT: Wan der Bruggen, Pierre
TILE REFERENCE: LUD 5881
CURRENT APPLICATION NUMBER: US/11/032,498
CURRENT APPLICATION NUMBER: US/11/032,498
PRIOR APPLICATION NUMBER: US 60/535,751
PRIOR APPLICATION NUMBER: US 60/535,751
PRIOR APPLICATION NUMBER: US 60/535,751
SERO ID NOS: 37
SOFTWARE: Patentin version 3.2
SEQ ID NO 36
LENGTH: 20
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Publication No. US20060008468A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR PELICATION NUMBER: 60/580,969
PRIOR FILING DATE: 2004-06-17
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: NY-ESO-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: artificial sequence
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US-11-155-288-7
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RESULT 6
US-11-072-512-2739
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APPLICANT:
APPLICANT:
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US-11-021-441-28

US-11-021-441-28

US-11-021-441-28

US-11-021-441-28

Sequence 28, Application US/11021441

Publication No. US2050249748A1

GENERAL INCRANION: US2050249748A1

APPLICANT: DUBENSKY, Thomas W., Jr.

APPLICANT: DUBENSKY, Thomas W., Jr.

APPLICANT: COCK, David N.

TITLE OF INVENTION: RECOMBINAT NUCLEIC ACID MOLECULES,

TITLE OF INVENTION: THEREOF

THEOR PILLING DATE: 2004-10-06

PRIOR APPLICATION NUMBER: US 60/599,377

PRIOR PILLING DATE: 2004-00-05

PRIOR PILLING DATE: 2004-00-30

PRIOR PILLING DA
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                                                                                                                                                                                         Query Match 100.0%; Score 47; DB 7; Length 180; Best Local Similarity 100.0%; Pred. No. 0.023; Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REPERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 412, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                 1 TVSGNILTIR 10
                        LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-485-517-412
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SEQ ID NO 7
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US-11-098-686-10549

US-11-098-686-10549

Sequence 10549, Application US/11098686

PUBLication No. US20060024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING

FILE REPREMENTE: 0953-128001

CURRENT APPLICATION NUMBER: US/11/098,686

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: US (0/416,395)

PRIOR PILING DATE: 2003-10-01

PRIOR PILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: PASSESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                           Length 223;
                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                           Query Match 74.5%; Score 35; DB 6; Best Local Similarity 70.0%; Pred. No. 8.1; Matches 7; Conservative 1; Mismatches 3
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR PILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SCOFTWARE: Patentin version 3.1
SEQ ID NO 412
LENGTH: 223
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                                                                                                                                                                                                                   ORGANISM: Staphylococcus epidermidis US-10-485-517-412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Lawsonia intracellularis
US-11-098-686-10549
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OTSUKI, TETSUJI
WAKAMATU, AI
SATO, HIROYUKI
ISHI, SHIZUKO
YAMAMOYO, JUB-ICHI
ISONO, YUUKO
HIO, YUUKO
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TAMECHIKA, ICHIRO
SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 77.8
Matches 7; Conservative
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APPLICANT: SUGIYAMA, TOMOJ
APPLICANT: GYGUXI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-:
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OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                 132 TVGGNIMKIR 141
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38 TLSGNILII 46
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                        1 TVSGNILTI 9
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APPLICANT: WALSH, ROGETICK T.
APPLICANT: WALSH, ROGETICK T.
APPLICANT: LO, Terence T.
APPLICANT: LO, Terence T.
APPLICANT: DI TERENCE: PI -0.044 PCT
CURRENT EDFORMSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REPRENCE: PI -0.044 PCT
CURRENT APPLICATION NUMBER: US/11/190,188
PRIOR APPLICATION NUMBER: US/10/220,382
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
PRIOR PRIOR DATE: 2001-03-01
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Pred. No. 40;
1; Mismatches 1; Indels
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                        APPLICANT: OLDOLA, DOLAGAMEN APPLICANT:
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
FELE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
FULE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US,11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
SOFTWARE: PATENTING DATE: 2001-11-05
INUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2739
LENGTH: 585
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US-11-190-188-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: INCTE GENOMICS, INC.
APPLICANT: TANG, Y. TOM
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: TRIBOULEY, Catherine
APPLICANT: IU, Dyung Anna M.
APPLICANT: YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/11190188
Publication No. US20060035331A1
GENERAL INFORMATION:
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POLICKY, Jennifer L.
AU-YOUNG, Janice
YANG, Junming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.3%;
77.8%;
YOSHIKAWA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.3
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 TPSGNILTL 395
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                   APPLICANT:
APPLICANT:
APPLICANT:
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Gaps .; 0

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                                                                                APPLICANT: CHIRON SpA
APPLICANT: FORTANA Maria Rita
APPLICANT: FORTANA Maria Rita
APPLICANT: PIZZA Mariagarazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR APPLICATION NUMBER: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NOS: 9218
SEQ ID NO 1556
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.2%; Score 33; DB 6; Length 426; 66.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.2%; Score 33; DB 6; Length 387; 77.8%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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Sequence 34, Application US/10873528

Sequence 34, Application US/10873528

Publication No. US20050276814A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M

TITLE OF INVENTION: Proteins
CURRENT APPLICATION NUMBER: US/10/873,528

CURRENT FILING DATE: 2001-01-26

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 388

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 34
US-10-467-657-1556
Sequence 1556, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7: Conservative
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Matches 6, Conservative
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45 SVAGNIITI
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19 TVSGNGLGIR
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LENGTH: 105
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                                   Sequence 901, Application US/10995561
Publication No. USZ0050272054a1
GENERAL INPORMATION:
APPLICAMT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDICANSCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559
TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559
TOTRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARRE: FasteseQ for Windows Version 4.0
SEQ ID NO 901
LENGTH: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Goedegebuur, Frits
APPLICANT: Goedegebuur, Frits
APPLICANT: Gualfetti, Peter
APPLICANT: Gualfetti, Peter
APPLICANT: Mefe, Paulien
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Stahlberg, Jerry
TITLE OF INVENTION: Callulases
FILE REFERENCE: G772-3
FILE REFERENCE: G772-3
FILE REPERENCE: G772-3
FRICH PILING DATE: 2003-08-15
PRIOR PLICATION NUMBER: US 60/458,696
PRIOR PLICATION NUMBER: US 60/458,696
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR FLING DATE: 2003-03-21
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR FLING DATE: 2003-03-21
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR PLICATION NUMBER: US 60/456,368
PRIOR PLICATION NUMBER: US 60/404,063
PRIOR APPLICATION NUMBER: US 60/404,063
PRIOR PLING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.2%; Score 33; DB 6; Length 471; 66.7%; Pred. No. 50; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 6; Length 517;
Pred. No. 56;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/10641678
Publication No. US20050277172A1
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-901
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RESULT 10
US-10-995-561-901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT Day, Anthony, G.
APPLICANT Goedegebuur, Frits
APPLICANT Gualfetti, Peter
APPLICANT Gualfetti, Peter
APPLICANT Mitchinson, Colin
APPLICANT Meefe, Paulien
APPLICANT: Sandgren, Mats
APPLICANT: Sandgren, Mats
APPLICANT: Stahlberg, Jerry
TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
TITLE OF INVENTION: Callulases
CURRENT APPLICATION NUMBER: US/10/641,678
CURRENT APPLICATION NUMBER: US 60/458,853
PRIOR PILING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-27
PRIOR FILING DATE: 2003-03-27
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US 60/456,368
                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-467-657-1358
US-10-467-657-1358
i. Sequence 1358, Application US/10467657
i. Publication No. US20050260581A1
i. GENERAL INFORMATION:
i. APPLICANT: FONTANA Maria Rita
i. APPLICANT: PIZZA Mariagrazia
i. APPLICANT: MASIGNANI Vega
i. APPLICANT: MANACI Elisabetta
i. TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
                                                                                                                           Score 32; DB 7
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/10641678
Publication No. US20050277172A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Neisseria gonorrhoeae
US-10-467-657-1358
                                                                                                                             68.1%;
80.0%;
                                                                                                       Query Match
Best Local Similarity 80.07
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Best Local Similarity 85.77
Matches 6; Conservative
                                                                                                                                                                                                             1 TVSGNILTIR 10
                                                                                                                                                                                                                                              19 TVSGNGLGIR 28
; SEQ ID NO 81
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-81
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95 TVSGNVL 101
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Gaps
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PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 77
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 523
TYPE: PRT
TYPE: PRT
ORGANISM: Irpex lacteus
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Matches 6; Conservative
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March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds (without alignments) 58.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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Maximum DB seq length: 2000000000
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1: geneseqp198
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:*

	Description	Aay06015 Human can			4	-		Adx08546 Class I H	Aay06068 Human can		Aay06065 Human can	Aay06064 Human can	Aay05986 Human can	Aay05978 Human can	Aay05979 Human can	Aau85105 Human NYN	Adk68648 Epitope l	Aaw62584 Cancer as	Aaw69665 Human NY-	Aay05965 Human can		Aay70862 Human tum	Aabo3154 Human oes	Aab69946 Human NY-	Aag67164 Amino aci
SUMMARIES	ID	AAY06015	AAY05969	AAB31331	AAE07734	ABG66802	ADG89596	ADX08546	AAY06068	AAY06066	AAY06065	AAY06064	AAY05986	AAY05978	AAY05979	AAU85105	ADK68648	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164
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مين	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang RF, Rosenberg SA; WPI; 1999-277270/23.

98WO-US019609. 97US-0061428P.

21-SEP-1998; 08-OCT-1997;

15-APR-1999.

Homo sapiens. WO9918206-A2. This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAXS6859). 30 Epitopes (see AAXO5988-Y060/17) were identified. The present peptide (ranked 28) corresponds to amino acid residues 53-62 of CAG-1 ORF1 (see AAXO5965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAXO5967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or

Cancer antigen NY ESO1/CAG-3.
Example 10; Page 42; 88pp; English.

	25	55	100	0	180	4	AAU01535	Aan	Aau01535	Human NY-	
	36	ď	0		0	4	A L C C O G G G	0 0		VM nemily	
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	17	ດ	100.0	٠.	087	Δ	AAU84818	Aans			
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	31	22	100.0	0.	180	9	ABU56508	Abu		Lung canc	
	32	22	100.0	٥.	180	y	ABU56694	Abu	Abu56694]	Lung canc	
	33	55	100.0	۰.	180	9	ABP74198	Abp	_		
	34	22	100	0.	180	9	ABU64816	Abue	_	Human NY-	
	35	22	100.0	0.	180	9	ABR83438	Abre	_	Human NY-	
	36	22	100	٥.	180	7	ADC09576	Adct	_	NY-ESO-1	
	37	52	100.0	٥.	180	7	ADD35564	Add3	_	Human NY-	
	38	22	100.0	0.	180	7	ADD35568	Add3		Human NY-	
	39	55	100.	0.	180	7	ADD25510	Add		Binding d	
	40	55	100	0	180	7	ADN39068	Adn ²	_	Cancer/an	_
	41	5	100.0	0	180	00	ADJ54139	Adi	_	Human NY-	
	4.2	, C	100		180	α	ADM72815	CEPA		Human NV-	
	. 4 . 4	, r.	100		180	α	ADM73418	Carpa Carpa	• -		_
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	4 4 4 7	n u			180	οα	ADM/341/ ADO18451	Adm/s	117	Human NY-	
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RES	RESULT 1										
AAY	AAY06015										
Ω	AAY06015		standard;		peptide;	je;	10 AA.				
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AC	AAY06015	015;									
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DŢ	16-AUG-1999	3-1999		(first	entry)	Ţ					
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OE	Human cancer	cance		antigen NY	NY	င်္ပ	ESO-1/CAG-3 HLA	A peptide motif.			
X								,			
¥	NY ESC	ESO-1/CAG-3	4G-3	gene	CAG-	ú.	gene; CAG-3 gene; cancer	r peptide; antigen; human;	human		
Ž	leukae	emia;	non	-Hodd)	cing]	Ĕ	leukaemia; non-Hodgkins lymphoma; Hodgkins	kins lymphoma, lung	cancer	ü	
K	metast	asis,	me]	Lanome	1; ade	, og	arcinoma;	ma; colon	Ϊ.		
¥	uterir	ne car	cer;	bre	ist ce	nce	uterine cancer; breast cancer; prostate cancer;	ovari	ncer;		
X	cervical	cal ca	incei	c; bla	dder	can	cancer; bladder cancer; kidney cancer;	y cancer; pancreatic cancer	: cance	er;	
K	liver	cance	er; E	sarcon	ום; בו	THOU	liver cancer; sarcoma; tumour; diagnosis;	immuno	therapy;		
Ž	vaccin	ne; hu	пеш	lenko	cyte	ant	vaccine; human leukocyte antigen; HLA.				
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The present sequence represents a cancer peptide that is based on amino acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-67), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or triumour antigen, antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an Ham molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcona, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
                                                                                                                                                                                         ö
without an HLA molecule. The cancer peptides form part of, or are derived
             from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NY ESO-1/CAG-3 gene, CAG-3 gene, cancer peptide, antigen, human, leukaemia, non-Hodgkins lymphoma, Hodgkins lymphoma; lung cancer, metastasis, melanoma; adenocarcinoma; thymoma; colon cancer, uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                         ö
                                                                                                                                                   Length 10;
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                                                                                                  Score 55; DB 2;
Pred. No. 0.6;
                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               AAY05969 standard; peptide; 10 AA.
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                                                                                                                                                100.0%;
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                                                                                                                                                                                     10; Conservative
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N-PSDB; AAX58600.
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                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                              Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  AAY05969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, osteoastromas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HIA binding protein are useful in the production
prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31302-59 represent exemplary antigens which are characteristic of tumours. They can be used to enhance the immune response of vaccines comprising peptides derived from human MAGE-A1 HIA (human leukocyte antigen) class II-binding protein. Peptides derived from the MAGE-A1 HIA binding protein stimulate the activity and proliferation of CD4+ I lymphocytes. The MAGE-A1 HIA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Exemplary antigen characteristic of tumours and derived from NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Der Bruggen P;
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine.
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                                                                                                 100.0%; Score 55; DB 2; Length 10;
100.0%; Pred. No. 0.6;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 32; 78pp; English.
                                                                                                                                                                                                                                                                                            AAB31331 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaux P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                             20-APR-2001 (first entry)
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                                                                                                                                      10; Conservative
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Best Local Similarity
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                                                                   Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000.
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                                                                                                   Query Match
                                 patient
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Matches
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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitopes) derived from the cancer antigen, NY 850-1. The MHC-II epitopes from NY 850-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given the generation and/or hapten and to induce tumour-specific humoral-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mediated immunity against cancer. The present sequence is MHC class I restricted human NY ESO-1 cancer peptide
                                                                                                                                                                                                  Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.6;
                                                                                                                                                           Human MHC class I restricted NY ESO-1 cancer peptide #2.
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                                    AAE07734 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001WO-US002765.
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                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang R, Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-496851/54.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                         immunotherapy
                                                                                                                                                                                                                                                                                                                                  Ното варіелв
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                                                                             AAE07734;
RESULT 4
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New polynucleotide capable of expressing an epitope-beta2m fusion protein useful for generating cytotoxic T lymphocyte responses against a tumor and in restoring antigen presentation in the tumor of a host.

Disclosure; Page 25; 46pp; English

Hunter M;

Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G,

WPI; 2002-508108/54

01-NOV-2001; 2001WO-GB004844. 02-NOV-2000; 2000GB-00026812. (ISIS-) ISIS INNOVATION LTD

WO200236146-A2.

10-MAY-2002.

Homo sapiens.

prostatic cancer; testicular cancer; lung cancer; breast cancer; malignant melanoma; mesothelioma; brain tumour; ovarian cancer; uterine cancer; cervical cancer; head and neck cancer; bladder cancer; Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma; acquired immunodeficiency syndrome; AIDS-related lymphoma.

human leukocyte antigen; fusion protein; epitope; cytostatic; tumour; gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer; liver cancer; biliary tract cancer; pancreatic cancer; vaccine;

Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;

Tumour antigen NY-ESO-1/CAG3 ORF1, HLA-A31 epitope.

(first entry)

24-SEP-2002

ABG66802;

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The invention relates to a new polynucleotide capable of expressing an epitope-beta 2m fusion protein useful for generating cytotoxic T lymphocyte (CTL) responses against a tumour or in reservania antigen presentation in the tumour of a host. Also included are a polynucleotide capable of expressing an epitope-beta_2m fusion protein in combination with a vaccination agent that stimulates a CTL response against the ceptope of the fusion protein for simultaneous, separate or sequential use in the treatment of cancer and a method of treating a tumour by administering a capable of expressing an epitope-beta 2m fusion protein, and optionally a vaccination agent that stimulates a CTL response against the epitope of the fusion protein. The polynucleotide is useful for generating CTL responses against tumours, for restoring antigen as gastrointestinal tumour, prostatic, testicular, lung or breast cancer, malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine as gastrointestinal tumour, prostatic, testicular, lung or breast cancer, cancer including cervical cancer, cancer of the head and neck, bladder cancer, Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and haematopoletic malignant tumours such as leukaemia and lymphoma. The headenstopoletic malignant tumours such as leukaemia and lymphoma. The epitope is an HLA (human leukocyte antigen) peptide derived from a viral or tumour antigen. The present sequence is a tumour HLA epitope used in the fusion proteins of the invention
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Best Local Similarity 100.
Matches 10; Conservative
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ABG66802 standard; peptide; 10 AA.

RESULT 5 ABG66802

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Conservative

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RESULT 6

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10-FEB-2005
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                                                                            Wang P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; infection; viral infections; virucide; bacterial infection; antibacterial; yeast infection; fungicide; fungal infection; protozoacide; cancer; cytostatic; melanoma; lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease; multiple sclerosis; neuroprotective; rheumaroid arthritis; antiarthritic; antirheumatic; systemic lupus erythematosus; antiinflammatory; dermatological; immunosuppressive.
                                                                                                                                                                                                                                                                             Identifying a cell that differentiates into a metastatic cancer cell, useful for preventing metastatic cancer, comprises identifying a mutated fibronectin in the cell.
                                                                                                                                                                                                                                                                                                                                      The invention comprises a method for identifying a cell that will differentiate into a metastatic cancer cell, the method involves identifying a mutated fibronectin in the cell. The method of the invention is useful for preventing metastatic cancer. The present amino acid sequence represents a Class I HLA-restricted testis cancer antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                    metastatic cancer cell differentiation; mutated fibronectin; metastatic cancer; class I HLA-restricted; testis; cancer antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 8; Length 10; 100.0%; Pred. No. 0.6;
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                                                                   Class I HLA-restricted testis cancer antigen #31
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 39; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADX08546 standard; peptide; 10 AA.
         ADG89596 standard; peptide; 10 AA.
                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                              28-MAY-2003; 2003WO-US016736.
                                                                                                                                                                                                  28-MAY-2002; 2002US-0383530P
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                                                                                                                    Unidentified
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                                                11-MAR-2004
                                                                                                                                                          04-DEC-2003
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                             ADG89596
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ADG89596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inverted microsomes from an animal cell (or its membrane fragments), in association with an externally disposed peptide antigen and a protein of the himent. The vaccine composition of the invention is useful for the prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast, fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The present amino acid sequence represents a class I HiA-restricted cancer antigen which was found to be expressed by normal spermatocytes and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention comprises a vaccine composition that consists of
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Pred. No. 0.6;
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                                                                                                                                                            (UNLO ) QUEEN MARY & WESTFIELD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 48; 83pp; English
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30-JUL-2004; 2004WO-GB003285
                                                                                    01-AUG-2003; 2003GB-00018096
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AAY06065;
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                                                                               This peptide corresponds to amino acid residues 53-63 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, utetine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide corresponds to amino acid residues 52-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY059678) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                             as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                                                                                                                                                                                                                    0; Indels
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                                                            Example 11; Page 50; 88pp; English.
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                                     Cancer antigen NY ESO1/CAG-3.
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            WPI; 1999-277270/23.
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Best Local Similarity
Matches 10; Conserv
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preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 2; Length 11; 100.0%; Pred. No. 0.66;
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                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAVOS965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAVOS966), portions of them and their CAG-3 ORF1, CAG-3 ORF2 (see AAVOS966), portions of them and their cancer recines the antiperse of cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cranspend animal; antisense oligonucleocides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods cancer peptide or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
                                                                                            NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostete cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                              Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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16-AUG-1999 (first entry)
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 W09918206-A2
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AAY05978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or arderived from, cancers such as primary or metaetistic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide corresponds to amino acid residues 50-62 of human NY ESO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                           Human cancer antigen NY ESO-1/CAG-3 peptide.
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                                                                                                                                                                                              AAY06064 standard; peptide; 13 AA.
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                                                                     3 ASGPGGGAPR 12
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Matches 10; Conserv
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The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAVO5965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2 (see AAVO5966), portions of them and their variants (see AAVO596-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods or preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Malanoma is treated by inducing cancer-specific T cells in vitro for subsequent
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; broater prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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Matches 10; Conservative
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                                                                                                                                                                        Homo sapiens
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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1 (See AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen, antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HIA molecule. The cancer peptides form part of, or are derived from, cancer peptimary or metastatic melanoma, thymoma, lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 64; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                       98WO-US019609.
                                                                                                                                                                                                                                          97US-0061428P.
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                                                                                                                                                                                                                                                                                                                 Wang RF, Rosenberg SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
                                                                         Homo sapiens.
                                                                                                                              WO9918206-A2
                                                                                                                                                                                                     21-SEP-1998;
                                                                                                                                                                                                                                        08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2002
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                                                                                                                                                                   15-APR-1999.
                                                                                              Synthetic.
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                                    vaccine
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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relativoship relative to their linked together in a different relativoship relative to their linked segments considered with the parent polypeptide and for induded are a function associated with the parent polypeptide and for induded are a synthetic polypeptide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymucleotides considered to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cospophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus and respiratory and respiratory syncytial virus), bacterial cuirus, Epstein-Barr virus and respiratory syncytial virus), bacterial cuirus, Epstein-Barr virus and respiratory syncytial virus), bacterial consumental, sinfluenza, Japanese encephalitis cuirus, infections caused by Neisseria, Meningococcal, Haemophilus, C. (e.g., infections caused by Plasmodium, Schistosoma, Toxoplasma and Giardial infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the
                                                                                                                                                                                                                                                                                                                                                       New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 27; 364pp; English.
                                                                                             25-MAY-2001; 2001WO-AU000622.
                                                                                                                                           26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                       (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                      Thomson SA, Ramshaw IA;
                                                                                                                                                                                                                                                                                WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                pathogen or cancer.
                                                                                                                                                                                                                                                                                                        N-PSDB; ABK36925.
WO200190197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
                                              29-NOV-2001
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10 ASGPGGGAPR 19

1 ASGPGGGAPR 10

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Gaps 0;

Query Match 100.0%; Score 55; DB 5; Length 30; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 10; Conservative 0; Mismatches 0; Indels

Search completed: March 13, 2006, 19:03:58 Job time: 77.2941 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-25 55 1 ASGPGGGAPR 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pirl: **
3: pirl: **
4: pirl: **

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	CREB-binding prote	aldose 1-epimerase	flagellar basal-bo	H+-transporting tw	XAA-PRO aminopepti	KIAA0641 protein -	myristylated alani	conserved hypothet	steroid hormone re			ര	Pur beta - human (competence/damage-	histocompatibility	hypothetical prote	probable transcrip	conserved hypothet		probable transfera	protein kinase sgg	polyketide hydroxy	probable protein k	(1->4)-alpha-D-glu	DNA-binding protei	protein kinase sgg	ovo protein - frui	apoptosis associat	Pex-related protei
	ID	T13828	C87425	AB3648		F82878	T00378	S08341	T36104	A29345		A87431	C72683		E87464	169006	T35619	F95899	F95307	G75580	T34842	835327	T35608	S10932	JC7726	A56038	S35423	S16356	T03748	C75445
	Length DB	!		173 2		357 2		335 2	436 2	521 2	679 2	954 2	··	• •	163 2		•	260 2	466 2	•	•••	575 2	•		757 2	1028 2	•	1213 2	1317 2	131 2
ا ا اع	Match 1	80.0	76.4	74.5	٠	74.5	74.5	72.7	72.7	72.7	72.7	72.7	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	٠.	70.9	£9.1
	Score	44	42	41	41	41	41	40	40	40	40	40	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	38
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44	Hypothetical Prote	hypothetical prote	alternative splici	alternative splici	alternative splici	related to antifre	alternative splici	proline iminopepti	hypothetical prote	POU-domain protein	hypothetical prote	syntaxin synt4 (im	class I histocompa	hypothetical prote	octamer binding tr
\$12246	AE3136	G98151	C40040	S26404	A40040	T51008	B40040	AC1965	T29031	S78452	T08459	T48847	180170	T30168	159234
~ .	N	N	N	N	~	N	N	N	~	~	~	~	~	~	0
161	Lαν	189	201	201	248	286	292	316	327	331	341	341	354	397	420
69.1	69.T	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1	69.1
w c							_	_	_	_	_	_	<u>~</u>	_	_
	χ Υ	38	38	38	38	38	38	33	36	38	36	38	ä	ñ	ĕ

ALIGNMENTS

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T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
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C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Akimaru, H; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>A;Residues: 1-3190 <AKI>A;Cross-references: UNIPROT: ONIS68; UNIPARC: UPI00003EB83; EMBL: U88570; NID:g1916929; P
C;Genetics:

A;Cross-references: FlyBase:FBgn0015624 A;Map position: X F;1723-1780/Domain: bromodomain homology <BRO>

Gaps ó Length 3190; Query Match 80.0%; Score 44; DB 2; Length 319 Best Local Similarity 77.8%; Pred. No. 1.8e+02; Matches 7; Conservative 1; Mismatches 1; Indels

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320 NGPGGGGPR 328 2 SGPGGGAPR 10 ò g

RESULT 2 C87425

Cyles 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
B;Jacenni, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo.
M.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Acesesion: C87425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1378 <STO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; A;Gene: CC1418 C;Superfamily: aldose 1-epimerase

76.4%; Score 42; DB 2; Length 378; 77.8%; Pred. No. 56; Query Match Best Local Similarity

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A;Residues: i-1207 <ISH>
A;Cross-references: UNIFARC:UPI000046CF7; EMBL:AB014541; NID:93327095; PIDN:BAA31616.1.,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myristylated alanine-rich protein kinase C substrate - bovine
NyAlternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
(Species Bos pringionius taurus (cattle)
C;Dete: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; $29270; A46098; PS0338
C;Accession: S08341; A32904; $29270; A46098; PS0338
Nucleic Acids Res. 17, 3967-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-335 <STU>
A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PII
A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PII
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-A;Reference number: A32904; MUID:89264553; PMID:2726763
           A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI0000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIAA0641 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-99,'Q',100-335 <ST2>
A;Cross-references: UNIPARC:UP1000017750A; GB:M24638; GB:M23738
                                                                                                                                                                                                                                                                         Length 357;
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                      Query Match 74.5%; Score 41; DB Best Local Similarity 77.8%; Pred. No. 74; Matches 7; Conservative 1; Mismatches
                                                                                                                                                                               A,Gene: pepp, UUS32
A,Genetic code: SGC3
C,Superfamily: X-Pro aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translation not shown A; Molecule type: mRNA
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S08341
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C;Species: Brucella melitensis
C;Accession: AB348
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazuc. M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesseroc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AB3548
A;Accession: AB3548
A;Accession: AB3548
A;Residues: 1-173 <KUR>
A;Residues: 1-173 <KUR>
A;Residues: 1-173 <KUR>
A;Accessiverimental source: strain 16M
C;Genetics:
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: F82878
R; Glass, O, I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 173;
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  Indels
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40;
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Pred. No. 61;
0; Mismatches
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Mismatches
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Similarity 80.0%;
8; Conservative
7; Conservative
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282 NGPSGGAPR 290
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                                            2 SGPGGGAPR 10
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Best Local Similarity
Matches 8; Conserv
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A; Map position: II
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Matches
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N.Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A29345; A49074
R;Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A;Title: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
A;Accession: A29345
A;Acce
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: 802165
R;Kaplan, J:B:/ bingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
J. Mol. Biol. 205, 71-83, 1989
A;Ritler Temporal regulation and overlap organization of two Caulobacter flagellar gene
A;Reference number: $02164; MUID:89178645; PMID:2648000
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: protein
A;Rosidues: 166-169, Xx,171-173 <WIL>
A;Rosidues: 166-169, Xx,171-173 <WIL>
A;Coss-references: UNIPARC:UPI000017AlDF
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;
E;174-434/Domain: ethab transforming protein homology <ERBA>
F;176-196/Region: zinc finger
F;212-236/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2; I
Pred. No. 1.4e+02;
1; Mismatches 1;
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A;Residues: 1-679 <KAP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.78;
77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                            steroid hormone receptor ERR1
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A; Residues: 191-253, SEF, 257-279, 283-292, 'V', 294,' PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Residues: 191-253,' SEF', 257-279, 283-292,'V', 294,' PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Residues: 191-253,' SEF', 257-279, 283-292,'V', 294,' PEQE', 299,'A', 300,'A', 302-313,'A', 315
B; Residues: 191-253,' SEF', 257-279, 283-288-298
B; Mannenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A; Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A; Reference number: A46098; MUID: 93216617; PMID: 8463217
R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Blochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protei
or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Accession: S29270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPARC:UPI000017750C
R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UP1000017750D; UNIPARC:UP1000017750B; UNIPARC:UP1000017750F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: brain
A,Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C,Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C,Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT: Q8CJX1; UNIPARC: UPI000017AD99; EMBL: AL049707; PIDN: CAB41270 A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riverby, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: 221597
A;Recession: T36104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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ilarity 77.8%;
Conservative (
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Best Local Similarity
Matches 7; Conserv
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C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45036
R;Bergemann, A.D.; Ma, Z.W.; Johnson, B.M.
Mol. Cell. Biol. 12, 5673-5682, 1992
A;Title: Sequence of CDNA comprising the human pur gene and sequence-specific single-str A;Reference number: A;5036; MUID:93078769; PMID:1448097
A;Accession: B45036
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-114 VBER.
A;Coss-references: UNIPROT:096QR8; UNIPARC:UPI000017C32D
A;Experimental source: HeLa cells
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon I. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Froc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2001
A.; Proc. Natl. complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUD:21173698; PMID:11259647
A; Accession: A87431
A; Residuaty
A; Molecule type: DNA
A; Residuats: preliminary
A; Residuats: 1-954 <STO>
A; Cross-references: UNIPROT:P15345; UNIPARC:UPI000012ABED; GB:AE005673; NID:g13422833; FC:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: C72683 S. S. Morikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; Kon DNA Res. 6, 83-101, 1999 sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropya A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-103 «KAW»
A;Cross-references: UNIPROT:09YDNO; UNIPARC:UPI000005DD18; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0884
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
Accession: C72683
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Pred. No. 2.4e+02;
0; Mismatches 2; Indels
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Pred. No. 49;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                              72.78;
77.88;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Competence/damage-inducible protein CinA [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: B87464
C;Accession: B87464
C;Accession: W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A.Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Molecule type: mRNA
A;Residues: 1-166 <RES.
A;Cross-references: UNIPROT:Q95518; UNIPARC:UPI00000892D6; EMBL:U02981; NID:g512971; PII
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C,Superfamily: uncharacterized protein related to CinA
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Best Local Similarity 77.8
Matches 7; Conservative
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AGGPGGGA 10
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A,Molecule type: DNA
A,Residues: 1-163 <STO>
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OBNY13 HUMAN PRELIMINARY;
OBNY13 HUMAN PRELIMINARY;
01-007-2000 (TrEMBLrel. 15, Ca
01-007-2002 (TrEMBLrel. 22, La
Hypothetical protein LAGE-2 (F
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Q67pj0
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         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening.";
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15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
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                                                                                  Q5bev2
Q6zv16
Q5x416
Q5vuq8
Q4fkf7
Q4sw43
Q4sw43
Q4sw23
Q4syu9
Q4tgy9
Q6uu52
Q4ilq5
Q96tz3
Q4wrl3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lethe B.G.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                    041LQ5_G1BZE
096T3_NEDCR
04WRL3_ASPFU
05BEV2_EMENI
05EV16_HUWAN
05K4L6_HUWAN
05K4L6_HUWAN
04SWQ8_HUWAN
04SWQ8_HUWAN
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Homo sapiens (Human).
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Nelson D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED sustation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                        Lethe B., Iucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T., "LAGE-1, a new gene with tumor specificity."; Int. J. Cancer 76:903-908(1998).
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                                                                                                                                                                                                                                                                                              MEDLINE=98430682; PubMed=9759882; Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.; Schwartzentruber D.J., Rosenberg S.A.; In the second of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.T.P.MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1; Length 180;
Pred. No. 2;
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; B122C5C2C8BE1569 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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Name=CTAG1-A, LAGE-2;
Homo sapiens (Human).
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EMBL; AF038567; AAD05202.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U87459; AAB49693.1; -; mRNA.
                                                                                                          MEDLINE=98289662; PubMed=9626360;
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100.0%;
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Q7LBY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                      CLEOTIDE SEQUENCE.
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                                                                                   TISSUE=Melanoma;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set of germ "DNA methylatic genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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MEDLINE=98289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.,
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethe B.G.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP277315; AAL27014.1; -; Genomic_DNA. EMBL; AJ278977; CAB76943.1; -; Genomic_DNA. EMBL; AJ278977; CAB76943.1; -; Genomic_DNA. EMBL; AF277315; AAL27013.1; -; Genomic_DNA. SEQUENCE 180 AA; 17992 MW; B122C5CZCGBE1569 CRC64;
                                                                                                                                                                            Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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Homo sapiens (Human).
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1 ASGPGGGAPR 10 |||| ||||| 53 ASGPRGGAPR 62

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                                              A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Troshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., NcKernan K.J., Malek J.A., Gunsarene P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X., Schein J.E., Jones S.J.M., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
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LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=LAGE-1B; Synonyms=LAGE-1L;

IsoId=O75638-1; Sequence=Displayed;

Name=LAGE-1A; Synonyms=LAGE-1S;

IsoId=O75638-2; Sequence=VSP_004301;

TISSUE SPECIFTCITY: Testis and very low level in placenta and in

some uterus samples. Observed in 25-50% of tumor samples of

melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Antigen; Polymorphism; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 1; Length 210;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W -> R. /
/FTId=VAR 007857.
8BE0EE00AE55E8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform LAGE-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> Q.
/FTId=VAR_007856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_004301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ223093; CAA11117.1; -; Genomic_DNA.
EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, AJ012835; CAA10194.1; -; mRNA.
EMBL, BC002835; AH028313.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSG0000126890; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA; 21120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          head and neck cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-InvDB; HIX0017163; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
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Best Local Similarity
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STRAIN=K96643;

X PubMed=15377794; DOI=10.1073/pnas.0403302101;

A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,

A Atkins T., Crosman L.C., Pit T., Churcher C., Mungall K.L.,

Bentley S.D., Sebainha M., Thomson N.R., Bason N., Beacham I.R.,

A Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,

Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Rabbinowitech B., Rutherford K., Sanders M., Simmonds M.,

Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,

Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,

T. Genomic plasticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pubbled=15377793; DO1=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
                                                                                                                                                                                                Putative lipoprotein.
OrderedLocusNames=BPSS2331;
Burkholderia pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.6%; Score 46; DB 2; Length 327; 88.9%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Lipoprotein.
SEQUENCE 327 AA; 33687 MW; AC5D2C7CC4A44A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia pseudómallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL. BX571966; CAH39817.1; -; Genomic_DNA.
GO; GO:0016620; C:membrane; IEA.
                                                                                                                                  Last sequence update)
Last annotation update)
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
                                  327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 AA
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                                     PRT;
                                                                                                      Created)
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                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative lipoprotein.
OrderedLocusNames=BMAA2092;
                           QG3HT9_BURPS PRELIMINARY;
Q63HT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q629N3 BURMA PRELIMINARY;
Q629N3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF04333; VacJ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AGGPGGGAP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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   BURPS
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0062 BUJ
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Gaps

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1; Indels

Pred. No. 36; 0; Mismatches

9; Conservative

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Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,

A Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,

Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,

Zafar N., Zhou L., Fraser C.M.;

"Structural flekibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).

RMBL; CP000011; ABU47030.1; -; Genomic_DNA.

RO, GO:0016020; C:membrane; IEA.

R InterPro; IPR007428; VacJ.

R Pfam; PP0433; VacJ; 1.

RRINTS; RR10805; VacJ; 1.

RRINTS; RR10805; VacJ; 1.

ROMDlete proteome; Lipoprotein.

R Complete proteome; Lipoprotein.

R SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cryptococcus neoformans var. neoformans JEC21.
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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Van Aken S., Fraser C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.6%; Score 46; DB 2; Length 330;
88.9%; Pred. No. 78;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Actin Cross-linking, putative.
ORFNames=CNC06000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708 AA
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InterPro; IPR001715; Calponin act_bd.
InterPro; IPR001715; Calponin act_bd.
InterPro; IPR002017; Spectrin.
Pfam; PF00307; CH; 2.
SWART; SM00033; CH; 2.
PR0SITE; PS00019; ACTININ 1; UNKNOWN 1.
PROSITE; PS00020; ACTININ 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.3"
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QŠKJMS CRYNE PRELIMINARY;
QSKJMS;
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A WICLEGE B.L., FW. T. Rowley D., Bruno D., Miranda M., Fukushima M., A Wickes B.L., FW J., Davis R.W.;

A Wickes B.L., FW. J., Davis R.W.;

T "Cryptococcus neoformans serotype D sequencing.";

Sumitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

L: CATUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

T "Cryptococcus neoformans serotype D sequencing.";

Sumitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

L: CATUTION: The sequence shown here is derived from an EMBL/ABY0100013; EAL21978.1; -; Genomic_DNA.

DR EMBL/ABY0100013; EAL21978.1; -; Genomic_DNA.

GO; GO: GO: SOO: Septemble act bd.

BR InterPro; IPR001992; EF-Hand "Eype.

BR InterPro; IPR001992; EF-Hand "Eype.

BR PROSITE; PS00019; ACTIMIN 1: UNKNOWN 1.

BR PROSITE; PS00020; ACTIMIN 2; UNKNOWN 1.

BR PROSITE; PS00020; ACTIMIN 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Pungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                                                        Gaps
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putrescine transport system permease protein.
Name-poll; OrderedLocusNames=BPSS0464;
Burkholderia perudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Beraproteobacteria; Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 708;
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708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;
Complete proteome. SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=CNBC1180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptococcus neoformans var. neoformans B-3501A.
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88.9%; Pred. No. 1.7e+02;
ive 0; Mismatches 1;
                                                                             83.6%; Score 46; DB 2; I
88.9%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                 708 AA.
                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                     RESULT 8
055WH CRYNE
1D Q55WH CRYNE PRELIMINARY;
AC Q55WH1;
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QG3N33;
                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                     47 AGGPGGGAP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 AGGPGGAP 55
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                                                                                                                                                                                                1 ASGPGGGAP 9
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                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=283643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28450;
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SEQUENCE 70
                                                                                Query Match
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GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR005790; DNA pol1II delta.
Pfam; PF06444; DNA pol3 delta; I.
TIGRFAMS; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                     362 AA; 38726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0400P8 HUMAN PRELIMINARY;
0400P8;
13-SEP-2005 (TrEMBLrel. 31, L.
13-SEP-2005 (TrEMBLrel. 31, L.
13-SEP-2005 (TrEMBLrel. 31, L.
PTGFRN protein (Fragment).
                                                                                                                                                                                  80.08;
                                                                                                                                                                                                                                                                                                                                                                                 QG2H22_BURMA PRELIMINARY;
Q62H22;
                                                                                                                                                                                  Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
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350 AAGPGGDAPR 359
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                                                                                                  Complete proteome. SEQUENCE 362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=13373;
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                                                                                                                                                               Query Match
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ID 0400P8_HU

AC 0400P8_T

DT 13-SEP-20

DT 13-SEP-20

DT 13-SEP-20

DT 13-SEP-20

DF PTGFN pp

GN Name=PTGF
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BURMA
                                                                                                                                                                                                     Matches
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A Atkins T. Crosgman L.C., Pitt T., Churcher C., Mungall K.L.,
A Bentley S.D., Sebaihia M., Thomson N.R., Bascham I.R.,
Brooks K., Brown K., Brown N., Charlis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
Peltwell T., Fraser A., Hance Z., Hauner H., Holroyd S., Jagels K.,
Rebinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Songsivial S., Stewns K., Tunapa S., Vesaratchavest M.,
Mitchead S., Yacts C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melicidosis,
Burkholderia pseudomallei.",
Broc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
REMBL; BX571965; CAH36946.11, -; Genomic DNA.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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25-007-2004 (TrEMBLrel. 28, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last sequence update)
Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BK571966; CAH37920.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00160215; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000515; BPD_transp.
PROSITE; PS50928; ABC_INI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 45; DB 2;
88.9%; Pred. No. 1e+02;
                    PubMed=15377794; DOI=10.1073/pnas.0403302101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15377794; DOI=10.1073/pnas.0403302101;
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0630T8 BURN
AC 0630T0
DT 25-0C
DT 25-0
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                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymeraes III, delta subunit (EC 2.7.7.7).
Name-holA; OrderedLocusNames=BMA2451;
Burkholderia anllei (FBeudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Burkholderia.
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InterPro; IPR005790; DNA pol1II delta.
Pfam; PF06144; DNA pol3 delta; I.
TIGREAMS; TIGR01128; hola, i.
Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 362 AA; 38726 MN; D5FF3DE783D41E41 CRC64;
                                                                          81.8%; Score 45; DB 2; Length 362;
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80.0%; Pred. No. 1.2e+02;
ive 1; Mismatches 1; Indels
DSFF3DE783D41E41 CRC64;
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Last annotation update)
                                                                                                                 Pred. No. 1.2e+02;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                               SEQUENCE
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Q6AV33 ORY
ID Q6AV3
AC Q6AV3
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                                                                                                                                                            Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riaugner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Baher N.K.,
Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Morley K.C., Hale S., Garrinci P., Prange C.,
Richards S., Worley K.C., Hale S., Garrinci P., Prange C.,
Whiting M., Madan P.J., Wadan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Butterfield W.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Marken D.N., Maran M.A.,
M. Marra M.A.,
M. Marken D.N., Maran M.A.,
M. Marra M.A.,
M. Marken D.N., Maran M.A.,
M. Marra M.A.,
M. Marken D.R.,
M. Marken D.R., Marken M.A.,
M. Marken D.R.,
M. Marken
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                            TISSUE=PCR rescued clones; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Myxococcaceae, Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 45; DB 2; Length 788;
88.9%; Pred. No. 2.6e+02;
Live 0; Mismatches 1; Indels
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Translation initiation factor 2.
ORFNames=AdehDRAFT_2230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BC09842; AAH98142.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR07110; Ig-like.
SMART; SM0040; Ig; 2.
SMART; PS50835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
TISSUE-PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4NUZ3_9DELT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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Matches 8; Conservative
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Homo sapiens (Human)
                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                    NCBI_TaxID=9606;
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Gaps
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                                                                                                                                     Gehalogeness 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larimer F., Land M.; "Annotation of Arthrobacter sp. "Annotation of the draft genome assembly of Arthrobacter sp. Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                           Larimer F., Land M.; "Annotation of Anaeromyxobacter" Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
ORFNames-ArthDRAFT 0188;
Arthrobacter sp. FE24.
Bacteria, Actinomycetales;
Micrococcineae; Micrococcaeae; Arthrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 271;
                                                                                                                                                                                                                                                                                                                                                                          Length 262;
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                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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EMBL; AAHGO1000033; EAL94269.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 271 AA; 29989 WW; SECC048B06CDDSBA CRC64;
                                                                                                                                                                                                                                                                                                                        262 AA; 25294 MW; 7EF93CC8DE0B47FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 44; DB 2; Le
87.5%; Pred. No. 1.3e+02;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; I
Pred. No. 1.2e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                            preliminary data.
EMBL; AAHD01000012; EAL79408.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE.
STRAIN=FB24;
US DOE Joint Genome Institute (PGF-ORNL);
                                                                      US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-FB24;
US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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QEAV33 ORYSA PRELIMINARY;
QEAV33;
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nes 7; Conservative
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nes 7; Conservative
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[2]
NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=290399;
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                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                      Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Haisao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., G.M., Salzberg S.L., Fraser C.M., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 44; DB 2; Length 367;
80.0%; Pred. No. 1.7e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Buell R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
Gramen; Q6X733; -.
Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; BBCG2D9D4CC18C86 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0063J18.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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Search completed: March 13, 2006, 19:14:23 Job time : 74.5882 secs

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Sequence 8, Appli
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Sequence 15, Appl
Sequence 9, Appli
Sequence 7, Appli
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Sequence 5, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 32326, A
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 117, App
Sequence 24923, A
Sequence 2759, A
Sequence 17831, A
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 3, Appli
Sequence 562, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                March 13, 2006, 19:14:49; Search time 18.5882 Seconds (without alignments) 44.477 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6
Sequence 6
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-751-798-8

US-09-341-828-9

US-09-341-829A-9

US-09-341-829A-7

US-08-791-495-5

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

US-09-341-829A-7

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US-09-341-829A-7

US-09-252-991A-17249

US-09-252-991A-17249
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US-09-270-767-43766
                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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                                                                                                                                              US-09-529-206E-25
55
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                        on:
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Sequence 31361, A Sequence 16, Appl Sequence 19543, A Sequence 11, Appl Sequence 20489, A Sequence 15052, A Sequence 20642, A Sequence 20642, A Sequence 2, Appli Sequence 18, Appli Sequence 18, Appli
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  3369, Ap
27111, A
32992, A
31361, A
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               Sequence
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US-10-104-047-3369
US-09-252-991A-27111
US-09-252-991A-31361
US-10-098-600B-16
US-09-249-002-376
US-09-249-002-376
US-09-249-002-376
US-09-249-002-376
US-09-252-991A-20489
US-09-902-540-12423
US-09-902-540-1252-91A-20642
US-09-902-540-1252-91A-20642
US-09-903-0048-2
US-09-904-016-7812
US-10-088-045-2
US-10-088-045-2
US-10-088-045-2
US-10-088-045-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02210
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                       US-08-836-620A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212.
REPERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 10; Conservative
  555
679
807
1207
1384
1388
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428
428
502
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518
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CLASSIFICATION: 435
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   CITY: 1
STATE:
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COUNTRY:
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                                                                                                     Sequence 8, Application US/08937263B
Sequence 8, Application US/08937263B
Setent No. 627445
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, All; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Churth, Alexander; Old, Lloyd of Jugd of TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer TITLE OF INVENTION: Associated Proteins, Uses Thereof, TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA TITLE OF INVENTION: Binding Peptides Derived Therefrom CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10103
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Fulbright & Jaworski, L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

SOFTWARE: WordDerfect

CURRENT APPLICATION DATA:

PAPPLICATION NUMBER: US/08/937,263B

FILING DATE: September 15, 1997

PRIOR APPLICATION UNMBER: 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORWATION:

NAME: Sinn, Eric, Patent Agent

REGISTRATION NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09751798; Patent No. 6525177; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Gaps
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100.0%; Pred. No. 2.7;
tive 0; Mismatches 0; Indels
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Sequence 25, Application US/09392714A

Patent No. 6688147

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gran's Ali O.
APPLICANT: Glare, Ali O.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE REFERENCE: LO46,17062

CURRENT APPLICATION NUMBER: US/09/392,714A

CURRENT PILLING DATE: 1998-09-09
ERALIER FILLING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH. 10.
COUNTALY.
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
AMDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION NUMBER: 09/725,182
APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
RECISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                             SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-392-714-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPE: amino acid
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Best Local Similarity
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<151> 1998-01-27
                                                                                                                                                                                    100.0%; Score 55; DB 2; Length 180; 100.0%; Pred. No. 2.7;
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APPLICANT: Lucas, Sophies
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf C----
STREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Glockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
                                                                                                                                                                                                                              0; Mismatches
                 NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
PRIOR APPLICATION NUMBER: PCT/US98/01445
                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 30, Application US/09849602
; Patent No. 6794501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                              10; Conservative
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                       1 ASGPGGGAPR 10
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                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Matches 10; Conserv
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Best Local Similarity
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                                                                                180
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LENGTH: 180
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US-08-791-495-7
                                                                                                                                                                                       Query Match
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                                                                                           APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND NHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 2; Length 180; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                           ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Thierry
TITLE OF INVENTION: LAGS-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE REFERENCE: LO461/706 (S/09/341,829A
CURRENT APPLICATION NUMBER: US 08/791,495 <151> 1997-0
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION: DATA:
                                                                                                                                                                                               NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING: DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                               STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09341829A
Patent No. 6794131
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 180 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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               US-09-165-546D-15
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
  : 600 Atlantic Avenue
Boston
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CORGANISM: Homo sapiens
US-09-341-829A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leth, Bernard
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPERENCE: LO461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.5%; Score 47; DB 2; Length 180; 90.0%; Pred. No. 30; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    85.5%; Score 47; DB 1; Length 180; 90.0%; Pred. No. 30; tive 0; Mismatches 1; Indels
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US-08-791-495-5

Sequence 5, Application US/08791495

Patent No. 5811519

GENERAL INFORMATION:

APPLICANT: Leth, Bernard

APPLICANT: Locas, Sophie

APPLICANT: Locas, Sophie

APPLICANT: Godelaine, Daniele

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES

CORRESPONDENCE ADDRESS: 14

CORRESPONDENCE ADDRESS:
                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASGPGGGAPR 10
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53 ASGPRGGAPR 62
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-341-829A-7
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US-09-341-829A-5
i Sequence 5, Application US/09341829A
j Sequence 5, Application US/09341829A
j Batent No. 6794131
j GENERAL INFORMATION:
APPLICANT: Leth, Bernard
j APPLICANT: Leth, Charles
APPLICANT: De Smet, Charles
APPLICANT: Boon-Fallent, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: LO461/7066
j CURRENT APPLICATION NUMBER: US 08/791,495
CURRENT PILING DATE: 1999-10-18
j PRIOR APPLICATION NUMBER: US 08/791,495
j RRIOR APPLICATION NUMBER: US 08/791,495
j NUMBER OF SEQ ID NOS: 14
j SOFTWARE: FastesEQ for Windows Version 3.0
j SEQ ID NO 5
j LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2; Length 210;
Pred. No. 34;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Length 210;
Pred. No. 34;
0; Mismatches 1; Indels
                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
PTLING DATE:
                                                                                                                                                                                                                                                                                            L0461/7005
                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 210 amino acids TYPE: amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 24923
LENGTH: 210
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APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039A
CURRENT TLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR PILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
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PRIOR FILING DATE: 1998-06-26
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PRIOR PLING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
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PRIOR APPLICATION NUMBER: US 09/105,839
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Pred. No. 1.1e+02;
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100.0%; Pred. No. ...
0; Mismatches
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ORGANISM: Pseudomonas aeruginosa
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80.0%;
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Best Local Similarity 100.'
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Best Local Similarity 80.0
Matches 8; Conservative
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US-09-252-991A-24923
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Sequence 117, Application US/09344040C

Sequence 117, Application US/09344040C

GENERAL INFORMATION:
APPLICANT: Dates, Ozlem
SAPPLICANT: Sahin, Ugur
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REPERENCE: LUD 556.1
CURRENT APPLICATION NUMBER: US/09/344,040C

CURRENT PILING DATE: 1999-06-25
FRIOR PILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 09/105,839
FRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 132

SEQ ID NO 117

SEQ ID NO 117
                                                                             FACENTE NO. 923-17-39.

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR PLICATION NUMBER: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32326
LENGTH: 421
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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                     Sequence 32326, Application US/09252991A Patent No. 6551795
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Patent No. 6673350
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 88.9%;
Matches 8; Conservative 0
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-344-040C-117
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US-09-833-039A-117
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Scoring table:

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; Publication No. US20040023314A1
; Fublication No. US20040023314A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
    TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR APLICATION NUMBER: 60/383,530
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
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US-11-144-912-27
US-10-296-734-1454
US-10-296-774-1436
US-10-295-077-388
US-10-188-332-141
US-10-146-473-69
US-10-117-937-75
US-10-16-734-834
US-10-657-022-75
US-10-657-022-75
US-11-067-04-75
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APPLICANT: Tafuro, Sabrina
APPLICANT: Meier, Ute-Christiane
APPLICANT: McMichael, Andrew James
APPLICANT: Ball, John Irving
APPLICANT: Ball, John Irving
APPLICANT: Hunter, Michael
TITLE OF INVENTION: Cancer Therapy
FILE REFERENCE: 5447.1001-000
CURRENT APPLICATION NUMBER: US/10/415,841A
CURRENT FILING DATE: 2004-01-21
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASELSEQ for Mindows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Peptide US-10-447-161-39
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. Sequence 52, Application US/10415841A

. Publication No. US20040131598A1

; GENERAL INFORMATION:
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Best Local Similarity 100.
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Sequence 52, Appl
Sequence 23, Appl
Sequence 102, App
Sequence 30, Appl
Sequence 8, Appli
Sequence 71, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 34, Appl
Sequence 386, Appl
Sequence 386, Appl
Sequence 139, Appl
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Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 74, Appl
Sequence 74, Appl
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                                                                                                          March 13, 2006, 19:51:56; Search time 60.4706 Seconds (without alignments) 69.096 Million cell updates/sec
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Sequence 11,
Sequence 11,
Sequence 15,
Sequence 11,
Sequence 11,
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cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-415-841A-52

US-10-125-841A-52

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US-10-482-029-202

US-09-751-798-8

US-09-751-798-8

US-10-026-06-3

US-10-026-06-3

US-10-026-06-3

US-10-026-06-3

US-10-026-074-832

US-10-296-734-832

US-10-296-734-832

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US-10-296-734-832

US-10-296-734-832

US-10-151-088-15

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US-10-877-373-9

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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-09-751-798-8

Sequence 8, Application US/09751798

Sequence 8, Application US/09751798

Patent No. US20020010321A1

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-teeng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8

CONTRESPONDER ADDRESS:
CONTRACTOR OF TRUNCALL F. TRUNCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 5; Length 179; 100.0%; Pred. No. 7.8;
                                                                                         100.0%; Score 55; DB 4; Length 30; 100.0%; Pred. No. 1.6;
                                                                                                                                                                 0; Indels
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage compuTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 202, Application US/10482029; Sequence 202, Application US/10482029; Publication No. US20050037445A1; GENERAL INFORMATION:
TITLE OF INVENTION: Oncology drug innovation; FILE REPERENCE: P 573 PC00; CURRENT APPLICATION NUMBER: US/10/482,029; CURRENT APPLICATION NUMBER: US/10/482,029; NUMBER OF SEQ ID NOS: 437; SOFTWARE: Patentin version 3.1; SEQ ID NO 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                 0; Mismatches
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APPLICATION NUMBER: US/09/751,798
; OTHER INFORMATION: NYSOla segment 4 US-10-296-734-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10, Conservative
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STATE: New York
COUNTRY: USA
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US-10-482-029-202
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US-10-482-029-202
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JUS-10-182-506A-23

Sequence 23, Application US/10182506A

Publication No. US20050136402A1

Sequence 23, Application US/10182506A

Publication No. US20050136402A1

APPLICANT: Wang, R-F

APPLICANT: Rosenberg, S A

APPLICANT: Rosenberg, S A

TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER

TITLE OF INVENTION: ANTIGEN, NY ESO-1

FILE REPERBURG: 217952

CURRENT APPLICATION NUMBER: US/10/182,506A

CURRENT PILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR APPLICATION NUMBER: 60/179,004

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.1

SEQ ID NO 23

LENGTH: 10
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i Sequence 1404, Application US/10296734

j Publication No. US2040054137A1

i Publication No. US2040054137A1

j APPLICANT: Thompson, Scott A

j APPLICANT: Thompson, Snuthetic molecules and uses therefor

j TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REPERBNCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT PILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 1404
                                                                                                                                                                                            Query Match 100.0%; Score 55; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 0.61; Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic US-10-182-506A-23
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Best Local Similarity 100.
Matches 10; Conservative
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                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                  US-10-415-841A-52
SEQ ID NO 52
LENGTH: 10
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Gaps

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Sequence 71, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDION DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REPERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. US20020164665Alman D. REGIGFRATION UNDRER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                  COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
OPERATING SYSTEME: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                  APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: CINKNOWN>
APPLICATION NUMBER: 08/725,182
FILING DATE: OCCOBER 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 318-3168 (ELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Blke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity
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Matches 10; Conser
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US-10-023-182-8
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Stockert, Standan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer;
; TITLE OF INVENTION: Antibodies Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HIA
Binding Peptides Derived Therefrom
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Blisabeth
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILLE OF INVENTION: Colon Cancer Antigen Panel
FILE PERERRECE: L0461/7105(ARV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321Alman D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Sequence 30, Application US/09849602
Publication No. US20030165834A1
                                                                                                            TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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US-09-849-602-30
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                                                                                                                                                                                                                                          TOPOLOGY: linear
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Best Local Similarity
Matches 10; Conserv
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us-10-29-02/-386

psequence 386, Application US/10295027

publication No. US200303350A1

sequence 386, Application No. US200303350A1

sequence 386, Application No. US200303350A1

APPLICANT: Adar, Daniel

APPLICANT: Adar, Daniel

APPLICANT: Ginsberg, Wendy M. APPLICANT: Ginsberg, Wendy M. APPLICANT: Ginsberg, Wendy M. APPLICANT: Ginsberg, Wendy M. APPLICANT: Marcad School School
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           APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TILLE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT APPLICATION NUMBER: US/02.04-04
PRIOR PELLING DATE: 2002-04-04
PRIOR PELLING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FRSESEQ for Windows Version 4.0
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CORGANISM: Homo sapiens
US-10-117-937-74
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US-10-295-027-386
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LENGTH: 180
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APPLICANT: KNUTH, Alexander
APPLICANT: OLD Lloyd
APPLICANT: OLD Lloyd
APPLICANT: Gnjatr. Sacha
TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
FILE REFERENCE: LUD 5726.1 CIP
FILE REFERENCE: LUD 5726.1 CIP
CURRENT PAPLICATION NUMBER: US, 10/34,614
PRIOR APPLICATION NUMBER: US, 60/355,828
PRIOR APPLICATION NUMBER: US, 60/355,828
PRIOR PLILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 14
LENGTH: 180
TYPE: PRT
CURRENT: Home sapiens
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Sequence 37. Application US/10026066
Publication No. US2030215425A1
GENERAL INFORMATION:
APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: EPITOBE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: EPITOBE SYNCHRONIZATION IN APPLICANT:
CURRENT FILING DATE: 2001-12-07
PRIOR PRILING DATE: 2001-12-07
PRIOR PAPLICATION NUMBER: 09/561,074
PRIOR PAPLICATION NUMBER: 09/561,675
PRIOR PAPLICATION NUMBER: 09/561,675
PRIOR PAPLICATION NUMBER: 09/561,572
PRIOR PAPLICATION NUMBER: 09/561,572
PRIOR PAPLICATION NUMBER: 09/561,571
PRIOR PLING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-117-937-74
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US-10-026-066-3
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APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Baiz, Natasha

APPLICANT: Bos Biotechnology, Inc.

ITILE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: Cancer

ITILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-11-08

PRIOR FILING DATE: 2001-11-08

PRIOR FILING DATE: 2001-11-13

PRIOR PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR FILING DATE: 2001-11-13

PRIOR PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR FILING DATE: 2001-11-3

PRIOR FILING DATE: 2001-11-3

PRIOR SEQ ID NOS: 207

SSC ID NO 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REPERSORS: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT PILING DATE: 2003-08-04
PRIOR PILING DATE: 2000-05-26
NUMBER: OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
LENGTH: 180
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; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 832, Application US/10296734 Publication No. US20040054137A1 GENERAL INFORMATION:
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Publication No. US20040076955A1
GENERAL INFORMATION:
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; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386
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US-10-296-734-832
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RESULT 2
US-11-021-441-28
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Sequence 28, Appl
Sequence 386, App
Sequence 3369, Ap
Sequence 66, Appl
Sequence 7722, Ap
Sequence 2722, Ap
Sequence 58, Appl
Sequence 58, Appl
Sequence 18, Appl
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Sequence 18, Appl
Sequence 18, Appl
Sequence 1845, Appl
Sequence 22845, A
Sequence 22663, A
Sequence 20556, A
Sequence 98, Appl
Sequence 9, Appli
Sequence 21887, A
Sequence 21887, A
Sequence 21887, A
Sequence 21887, A
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                                                                                                                                                                                                                                               March 13, 2006, 19:54:06; Search time 6.82353 Seconds (without alignments) 40.793 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-021-441-28
US-11-072-1512-3369
US-11-072-512-3369
US-11-072-512-3369
US-11-072-512-3295
US-11-072-512-3295
US-11-240-769-58
US-10-508-892-2
US-10-508-892-2
US-11-240-769-58
US-10-508-892-2
US-11-223-294-54
US-11-072-512-32845
US-11-096-568A-22845
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US-11-096-568A-22693
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US-11-096-568A-22693
US-11-096-568A-28887
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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26 37 67.3 198 7 US-11-096-568A-22493 Sequence 22494, A 28 37 67.3 269 7 US-11-096-568A-22493 Sequence 22493, A 29 37 67.3 379 7 US-11-096-568A-382 Sequence 16, Appl 30 37 67.3 401 7 US-11-096-568A-381 Sequence 382, Appl 31 37 67.3 410 7 US-11-096-568A-381 Sequence 1792, Appl 32 37 67.3 1465 7 US-11-096-568A-381 Sequence 1792, Appl 33 37 67.3 1465 7 US-11-096-568A-181 Sequence 1792, Appl 34 37 67.3 1465 7 US-11-096-568A-191 Sequence 1059, Appl 35 56.4 167 7 US-11-096-568A-1910 Sequence 10542, Appl 36.5 66.4 167 7 US-11-096-568A-1910 Sequence 21910, Appl 36.5 66.4 280 7 US-11-143-980-34 Sequence 15, Appl 40 86.5 155 7 US-11-143-811 Sequence 15, Appl 41 36 65.5 155 7 US-11-143-81-3 Sequence 15, Appl 42 36 65.5 188 6 US-10-096-568A-1910 Sequence 19104, Appl 43 65.5 188 6 US-10-096-568A-19104 Sequence 19104, Appl 43 65.5 188 6 US-10-096-568A-19104 Sequence 19104, Appl 44 36 65.5 238 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10553, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10554, Appl 44 36 65.5 246 7 US-11-194-890-12 Sequence 10554, Appl 44 36 65.5 246
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ALIGNMENTS

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MESULT 2

RESULT 2

Sequence 7, Application US/11155288

Sequence 7, Application US/11155288

Publication No. USZOSOGO4668A1

SERVICANT: Chiang, Chih.-Beng
APPLICANT: Chiang, Chih.-Beng
TITLE OF INVENTION: COMEINATION:
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION: COMEINATION: USANOSTICS FOR VARIOUS TYPES OF CANCERS
CURRENT FILING DATE: 2005-06-17

NUMBER OF SEQ ID NOS: 40 06-17

SEQ ID NOS: 40 06-17

GREEN FRICK FOR WINDOW VETSION 4.0

SEQ ID NOS: 40 06-17

GREEN FRICK FOR WINDOW VETSION 0.0 35;

MATCHES 10; CORSELVATIVE 0, MISMATCHES 0, Indels 0, Gaps 0;

OV 1 ASCENCIARR OF SEQ ID NOS: 40 06-17

SEQUENCE 28, APPLICATION USZOSOSY 740-11

Publication No. USZOSOSY 740-11

Publication No. USZOSOSY 740-10

MAPPLICANT: OF INVENTION: EXPRESSION CASSETTES, AND METHODS OF USE TITLE OF INVENTION: EXPRESSION CASSETTES, AND METHODS OF USE TITLE OF INVENTION NOMBER: US/11.021, 41

CORRERANT FILLIA DATE: 2004-10-26

FILLS REFRENCE: 281.700390

CURRERY FILLE OF INVENTION NOMBER: US/11.021, 41

FRIOR FILLY OF DATE: 2004-10-06

FRIOR FILLY OF DATE: 2004-10-06
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Sequence 66, Application US/11037243; Publication No. US20050287546A1; GENERAL INFORMATION:
                                                                                      TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 ASGPGSGSP 481
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US-11-072-512-3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-11-072-512-3295
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                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-10-623-155-496

Sequence 496, Application US/10623155

Sequence 496, Application US/10623155

Publication No. US20050261166A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSIS OF LUNG CANCER

TITLE OF INVENTION: COMPOSIS OF LUNG CANCER

TITLE OF INVENTION: NUMBER: US/10/623,155

CURRENT APPLICATION NUMBER: US/10/623,155

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 55; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-08-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-06-30
PRIOR PRILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
SOFTWARE: PABLES OF UNOS: 129
SOFTWARE: PABLES OF UNOS: 129
SOFTWARE: PABLES OF WINDOWS VERSION 4.0
SEQ ID NO 28
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Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: STATO, HERSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHIT, SHIZUKO
APPLICANT: ISHIT, SHIZUKO
APPLICANT: ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.2
Best Local Similarity 100.
Matches 8; Conservative
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13 ASGPGGGA 20
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US-11-072-512-3369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.5%; Score 41; DB 7; Length 953; Best Local Similarity 87.5%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 1; Indels
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SCOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: GENEBEEL, SEAN
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHARYDCEAK, GLEN
APPLICANT: CHARYDCAK, GLEN
APPLICANT: CHARYDCAK, GUCHA
ITILE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/11/037, 243
CURRENT APPLICATION NUMBER: US/09/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOOTWARRE: Patentin Ver: 2.1
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70.9%; Score 39; DB 7; Length 213; 100.0%; Pred. No. 63; 1ive 0; Mismatches 0; Indels
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APPLICANT: SOPPET et al.

TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REPERENCE: PZ037PLC2

CURRENT APPLICATION NUMBER: US/11/240,769

CURRENT FILING DATE: 2005-10-03

PRIOR PILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 09/997,131

PRIOR FILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-07-08

PRIOR PILING DATE: 1999-02-10

PRIOR FILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 173

SOFTWARE: PETENTING VET: 2.0

SEQ ID NO 58

LIENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARR: PATENTIN VET: 2.1
SOFTWARR: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TAMECHKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OFSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVel full length cDNA
                       Sequence 2722, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-11-240-769-58
Sequence 58, Application US/11240769
Publication No. US20060036089A1
GENERAL INFORMATION:
                                                                                        APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
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IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                         OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-11-072-512-2722
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ORGANISM: Homo sapiens
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Matches
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Pred. No. 2.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%; Score 40; DB 7; Length 678; 77.8%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B.P
CURRENT FILING DATE: 2005-03-22
NUMBER OF FILING DATE: 2005-03-22
NUMBER OF FILING DATE: 2005-03-22
NUMBER OF FILING DATE: 2005-03-22
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT: APPLICANT: SERI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSURA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
CURRENT PILIKO DATE: 2005-03-07
CURRENT FILING DATE: 2005-03-07
PRIOR PELING DATE: 2002-01-25
PRIOR PELING DATE: 2001-15
PRIOR PELING DATE: 2001-15
PRIOR PELING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 3295
LENGTH: 678
Sequence 3295, Application US/11072512
Publication No. US20060029945A1
                                                              APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
                                                                                                                                                                                                                                                                                               NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKWA, TSUTOMU
OTSUKA, MOTOYUKI
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77.88;
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US-11-087-099-7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.7
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                    HIO, YURI
OTSUKA, KAORU
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1051 SGSGGGSPR 1059
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US-11-072-512-3295
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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, ORGANISM: Human
US-11-223-294-54
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     LENGTH: 430
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US-10-508-892-2
Sequence 2, Application US/10508892
Sequence 2, Application No. US20060014218A1
GENERAL INFORMATION:
APPLICANT: Golz, Stefan
APPLICANT: Weingartner, Bernhard
APPLICANT: Weingartner, Bernhard
TITLE OF INVENTION: Neuropeptics and Therapeutics for Diseases Associated
TITLE OF INVENTION: Neuropeptics and Therapeutics
FILE REPERENCE: Le A 35 944
CURRENT APPLICATION NUMBER: PO14-09-22
PRIOR APPLICATION NUMBER: PO2006654.4
FRICR APPLICATION NUMBER: EP 02006654.4
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2003-03-14
SPIOR PAPLICATION NUMBER: EP 02006654.4
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10992577
Publication No. US20050260687A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gores, Kenneth A.
APPLICANT: Borowsky, Beth B.
ITLE OF INVENTION: DAMES A.
TITLE OF INVENTION: DAMES Thereof
FILE REFERENCE: 57155-D/JW
CURRENT APPLICATION NUMBER: US/09/92,577
CURRENT APPLICATION NUMBER: US/09/538,036
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 71
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; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-240-769-58
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                               Query Match 70.9%; Score 39; DB 7; Length 233; Best Local Similarity 87.5%; Pred. No. 68; Matches 7; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 77.8
Matches 7; Conservative
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LENGTH: 430
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Publication No. US2005026147741

GENERAL INFORMATION:

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: CHAMPION, BRIAN ROBERT

APPLICANT: TUGAL, TAMARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS

TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

TILLE OF INVENTION NUMBER: US/11/078,735

CURRENT PILING DATE: 2005-03-10

PRIOR APPLICATION NUMBER: PCT/GB03/03908

PRIOR PILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-09-04

PRIOR PILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: PCT/GB03/03285

PRIOR PILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: PCT/GB03/0334.2

PRIOR APPLICATION NUMBER: PCT/GB03/0534.2
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                                                                             Length 430;
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                                                                          Score 39; DB 6; Pred. No. 1.1e+02;
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NESOLA 12

SEQUENCE 54, Application US/11223294

SEQUENCE 54, Application US/11223294

SEQUENCE 54, Application US/11223294

SEQUENCE 50.22006003332A1

SEDICANT: VOSHIDA, Hiromi

APPLICANT: VOSHIDA, Hiromi

APPLICANT: HABATA, YUGO

APPLICANT: HABATA, YUGO

TILLE OF INVENTION: NOVEL RFRP-3 And Its DNA

FILE REFRENCE: 2944USOP

CURRENT APPLICATION NUMBER: US/11/223,294

CURRENT APPLICATION NUMBER: US/10/487,634

PRIOR APPLICATION NUMBER: PCT/JP02/08466

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2000-09

PRIOR FILING DATE: 2000-09

PRIOR FILING DATE: 2000-09

PRIOR FILING DATE: 2000-09

NUMBER 0F SEQ ID NOS: 78

SEQ ID NO 54
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
US-10-508-892-2
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WENGUT: 14

US-11-050-346-63

Sequence 63, Application US/11050346

Publication No US20060002924A1

GENERAL INFORMATION:

APPLICANT: BODNER, WARK WILLIAM

APPLICANT: CHAMPTON:

APPLICANT: TURNARD, ANDREW CHRISTOPHER

APPLICANT: TURNARD, GORGE ALBERT

TITLE OF INVENTION: THEIR USE IN MEDICAL TREATMENT

TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND

TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING

CURRENT FILING DATE: 2003-05-20

PRIOR PILING DATE: 2003-05-24

PRIOR PILING DATE: 2003-05-24

PRIOR PELING DATE: 2003-05-24

PRIOR PELING DATE: 2003-05-04

PRIOR PELING DATE: 2002-09-07

PRIOR PELING DATE: 2002-09-07

PRIOR PELING DATE: 2002-09-07

PRIOR PELING DATE: 2002-09-10

PRIOR PELING DATE: 2002-0
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PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/GB02/05133
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 18
LEGGTH: 618
LEGGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-078-735-18
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; ORGANISM: Homo sapiens
US-11-050-346-63
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| NESULT 18
| Sequence 18, Application US/11103077
| Publication No. US20060003927A1
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Human

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The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AXV55967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of
                                                                                                                                                                                                                                                                                                                                                               NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metaetasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                             Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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Wang RF, Rosenberg SA;
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AAu85105
AAw685105
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Aay70562
Aay03154
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AAY52430
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ABR48210
ABU56508
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seq length: 200000000
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Database

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Title:

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Lung canc Lung canc Human NY-Human NY-Human NY-

ABP74198 ABU64816 ABR83438 ADC09576

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derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific I cells in vitro for subsequent
                         cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are
      the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
                                                                                                                                                                                                                                                                       return to a patient
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Sequence 15 AA;

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Score 78; DB 2; Length 15;
Pred. No. 0.0029;
Mismatches 0; Indels
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    100.08;
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 Query Match
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Matches 15; Conservative
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Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide. AAY05979 standard; peptide; 20 AA (first entry) 16-AUG-1999 RESULT 2

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; overstate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine.

Bapiens. WO9918206-A2 15-APR-1999 Synthetic

21-SEP-1998;

USSH) US DEPT HEALTH & HUMAN SERVICES. 97US-0061428P 08-OCT-1997;

Rosenberg SA; Wang RF,

WPI; 1999-277270/23.

Cancer antigen NY ESO1/CAG-3.

Claim 16; Page 64; 88pp; English.

The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05955), as new and potent tumour antigen capable of eliciting an antigen specific immune response by T cerls. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked cogether in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypucides the synthetic polypeptides and polynucleotides or synthetic polypeptides. The synthetic polypeptides and polynucleotides synthetic polypeptides. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, break, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, and neck, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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linkage in the parent polypeptide, for inducing immune response against a
                              cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New synthetic polypeptides having several different segments of at least
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
HLA molecule. The cancer peptides form part of, or are derived from,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 27; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU85105 standard; peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma; Toxoplasma; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NYNSOla segment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomson SA, Ramshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen or cancer
                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK36925.
                                                                                                                                                                                                                                                                                           Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200190197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU85105;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                              patient
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunocherapy. The invention is also useful for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protoxoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the host. The present sequence is that of a protein which is related to the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer associated antigen; NY-ESO-1; regression; progression; onset;
                                                                                                                                                                                                                                                     100.0%; Score 78; DB 8; Length 179; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knuth A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gure A, Old LJ, Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW62584 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00725182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US016335
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                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                       1 AGAARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                        47 AGAARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-286417/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV38566
                                                                                                                                                                                                                       Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drijfhout JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9814464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW62584;
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                            AAW62584
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     888888888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the aubstrate permits processing by a proteasome; contacting the aubstrate with a composition including the proteasome; under conditions that support processing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for protezoacide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation,
                                                                                       is
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Bestein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence a peptide derived from a parent protein used to construct a savine of
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       ö
                                                                                                                                                                                      Length 30;
                                                                                                                                                                     Score 78; DB 5; Lengta J. Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epitope liberation-related NY-ESO-1 protein SegID11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ADK68648 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qiu Z,
                                                                                                                                                                                                                       ö
                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001; 2001US-0336968P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2002; 2002US-00292413
                                                                                                                                                                                                                                                       1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                      AGAARASGPGGGAPR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMARD J J L.
DIAMOND D C.
QIU Z.
LEI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-167209/16.
                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADK68674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003228634-A1.
                                                                                                                                                     Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simard JJL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2003
                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                         ADK68648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SIMA/)
(DIAM/)
(QIUZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEIX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
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                 The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 2; Length 180;
Pred. No. 0.027;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                             therapeutic regime
                                                                                                                                                                                                                                                                                                       Sequence 180 AA;
*888888888888
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Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                               Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
                            AAW69665 standard; protein; 180 AA.
                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                      98WO-US001445.
                                                                                                                                  97US-00791495.
48 AGAARASGPGGGAPR 62
                                                   (first entry)
                                                                                    Homo sapiens.
                                                                                                WO9832855-A1.
                                                                                                                      27-JAN-1998;
                                                                                                                                  27-JAN-1997;
                                                   27-0CT-1998
                                                                                                           30-JUL-1998
                                        AAW69665;
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The present sequence represents human NY-ESO-1, formerly known as IL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, Example 2; Page 57-58; 73pp; English tumours. particularly

Godelaine D, Boon-Falleur T;

De Smet C,

Lethe B,

1998-427951/36. Lucas S,

N-PSDB; AAV50348

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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human 850-1/CAG-3 (or CAG-3) gane. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), an extended to provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antibodies reacting with the CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer beptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, lymphoma, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine as uch as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
                       enrich
T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enter isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                          100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05965 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US019609.
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                                                                                                                                                                                                                                                                            1 AGAARASGPGGGAPR 15
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                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                     AGAARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-277270/23.
N-PSDB; AAX58599.
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                       Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1998;
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                                                                                                                                                                                                                                     Matches
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AAY05965
      88888888
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This sequence represents a human tumour antigen, NY-ESO-1, the cDNA individual and sisolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and cumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY ESO-1 are bound by both MHC (major histocompactibility complex) class I and class I molecules for presentation to T-cells. Peptides AAY52431-Y52434 bind to Class I HIA-AZ molecules, thereby stimulating to class II HIA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells
                                                                                                                                                                                                                                                       HLA
                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Peptide (AAY52434) presented by MHC Class I HLA-
                                                                                                                                                                                                                                    .153
== "Peptide presented by MHC Class I HLA-A24 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                  /note= "Peptide presented by MHC Class I HLA-A24"
                                                                                                                                                                                                                                                                                                        "Peptide presented by MHC Class I HLA-B52"
                                                                                                                   /note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                        "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                       'note= "Peptide presented by MHC Class I HLA-B52"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                         .166
e= "Peptide presented by MHC Class I HLA-A3"
                                                'note= "Peptide presented by MHC Class I HLA-A3"
                                                                                                                                                                                     "Peptide presented by MHC Class I HLA-B8"
                                                                                                                                                                                                                    'note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Peptide presented by MHC Class I HLA-A3"
                    "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen Y, Scanlan M, Alexander K,
                                                                                   presented by MHC Class
                                                                  118. .126 /
/note= "Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
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98US-00165546.
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                                                                                                 .133
                                  .124
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                    'note=
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                                                                                                                                                                                                                                                                                                      'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-038483/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stockert E, Jager
Gure A, Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9953938-A1.
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/note= "Peptide presented by MHC Class I HLA-B5 and HLA-B55"
B52"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84. .92
/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytocoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                    Gaps
treated by inducing cancer-specific T cells in vitro for subsequent return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .91
:e= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110. .118
'note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Peptide presented by MHC Class I HLA-B44"
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== "Peptide presented by MHC Class I HLA-B7"
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e= "Peptide presented by MHC Class I HLA-B7"
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/note= "Peptide presented by MHC Class I HLA-A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Peptide presented by MHC Class I HLA-B7"
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                                                                                100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .68
.e= "Peptide presented
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                                                                                                                                                                                                                                                                  AAY52430 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     Human tumour antigen NY-ESO-1.
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                                                                                                                                                1 AGAARASGPGGGAPR 15
                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .108
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                                                                                                                                                                              48 AGAARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .104
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                                                Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Unidentified
                                                                                                                                                                                                                                                                                                                                  21-OCT-2004
15-PEB-2000
                                                                                                                                                                                                                                                                                                     AAY52430;
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AAB03154 standard; protein; 180 AA.

RESULT 10

AAB03154

48 AGAARASGPGGGAPR 62

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                                                                                                                                                                                                                                                                                                                                                                                          NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
               Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                 Gaps
                                                                                                               ;
                                                                               Length 180;
                                                                                                             0; Indels
                                                                             Score 78; DB 3;
Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klade C;
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOEH ) BOEHRINGER INCELHEIM INT GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 62-63; 73pp; English.
                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                          AAY70862 standard; protein; 180
                                                                            Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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                                                                                                                                             1 AGAARASGPGGGAPR 15
                                                                                                                                                                Aarnoudse CA,
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N-PSDB; AAD00152.
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                                               Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                          31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schrier PI,
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                                                                                                                                                                                                                                                                                          AAY70862;
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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma coll lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The antigen is useful as an immunogen when combined with an adjuvant, in both precursor and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions,
                                                                                                                     Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                 note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                   note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Potential O-phosphorylation site"
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                                                                                                                                                                                                                                                                                               note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                              /note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Potential transmembrane domain"
                                                                                    Human oesophageal cancer-associated antigen NY-ESO-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Y, Tureci O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                              Location/Qualifiers
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                                                  23-OCT-2000 (first entry)
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N-PSDB; AAA61483.
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                                                                                                                                                                                             Homo sapiens
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                   AAB03154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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Gaps

; 0

Query Match 100.0%; Score 78; DB 3; Length 180; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 15; Condervative 0; Mismatches 0; Indels

1 AGAARASGPGGGAPR 15

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AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                            AAG67164;
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AAU01535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.
targetted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scanlan M;
                                                                                      Score 78; DB 3; Length 180;
Pred. No. 0.027;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knuth A,
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(SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                              AAB69946 standard; protein; 180 AA.
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                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0,
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                                                                                                                                                                                                                                                                                                                                                                                   Human NY-ESO-1 protein.
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                                                  Sequence 180 AA;
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                                                                                                                                                                                                                                            RESULT 11
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NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; human leukocyte antigen-determining region; disease progression;
                                                                                                                                                                                                                                                                                                                                                                              Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukcoyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumors.
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                                                                                                                                                                                                                                                                                                                          Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
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                                                                                                                                                AAG67164 standard; protein; 180 AA.
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AGAARASGPGGGAPR 62
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Gaps

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Query Match 100.0%; Score 78; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 15; Conservative 0; Mismatches 0; Indels

Human, major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitops; MHC-I epitope; cancer antigen; NY ESO-1 protein; CD4 T lymphocyte; human leucocyte antigen; tumour-specific humoral-mediated immunity; cancer; cytostatic;

(first entry)

06-NOV-2001

AAE07714;

Human NY ESO-1 protein

45. .47 /note= "Encoded by CCCGGGGC"

Location/Qualifiers

Misc-difference

immunotherapy

Homo sapiens

WO200155393-A2

02-AUG-2001

us-09-529-206e-26.rag

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The sequence represents a human NY-ESO-1 tumour rejection antigen precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC class II HLA-DR NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.
disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.
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138
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Best Local Similarity
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                                                     Homo sapiens
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New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

Example 1; Fig 1; 134pp; English.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

26-JAN-2001; 2001WO-US002765. 28-JAN-2000; 2000US-0179004P. 29-SEP-2000; 2000US-0237107P. ö

Rosenberg SA,

Wang R,

N-PSDB; AAD14179, AAD14180.

WPI; 2001-496851/54.

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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NT ESO-1. The MHC-II epitopes (TC mon NV ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DR creatricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1
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Gaps

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1 AGAARASGPGGGAPR 15

62

48 AGAARASGPGGGAPR

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AAE07714 standard; protein; 180 AA.

RESULT 14 AAE07714

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AAU84818;
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(first entry) 08-MAY-2002

Human NYNSOla consensus sequence.

Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonnella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.

Homo sapiens.

WO200190197-A1

29-NOV-2001

25-MAY-2001; 2001WO-AU000622.

26-MAY-2000; 2000AU-00007761

(AUSU) UNIV AUSTRALIAN NAT.

Ramshaw IA; Thomson SA,

WPI; 2002-147575/19.

New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.

Example 3; Fig 27; 364pp; English.

The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked to geveral different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypuclectide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymuclectides concer (synthetic polypeptides. The synthetic polypeptides are a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus (such as infections caused by Neisseria, Meningococcal, Haemophilus, cvirus, Epstein-Barr virus and respiratory syncytial virus), bacterial color, infections caused by Neisseria, Meningococcal, Haemophilus, cvirus, Epstein-Barr virus and respiratory syncytial virus), bacterial color, virus, batterial and Mycobacterium or paraaitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a consensus sequence for a parent protein used to design a savine of the

Sequence 180 AA;

Gaps ő 100.0%; Score 78; DB 5; Length 180; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0

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1 AGAARASGPGGGAPR 15 62 AGAARASGPGGGAPR

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Search completed: March 13, 2006, 19:03:59 Job time : 113.941 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24; Search time 17.8235 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

1 AGAARASGPGGGAPR 15 US-09-529-206E-26 78 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR, 80:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

82 2 T04476 222 136115 566 2 T21096 692 2 T21096 692 2 T21095 220 2 E72464 1690 2 T35694 333 2 C46433 504 2 A35646 513 2 C46433 627 2 A44112 627 2 A44112 627 2 A44112 627 2 A44112 627 2 A44112 628 2 A44010 259 2 A44010 269 2 A4901 309 2 A99169 319 1 A46013 309 2 A4901 309 2 A9169 319 2 A47008 269 2 A4901 309 2 A9169 319 2 A47008 250 2 A4901 309 2 A9169 319 2 A47008 319 2 A47008	Score	* Query Match	Length	DB	SUMMARIES	Description
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61.5 1690 2 T35694 60.3 3380 2 C46451 59.0 304 2 AB5526 57.7 275 2 C84673 57.7 275 2 C84673 57.7 627 2 C84673 57.7 627 2 C84673 57.1 730 2 A36233 57.1 730 2 A36233 56.4 226 1 S51660 56.4 259 2 A44088 56.4 269 2 A44088 56.4 269 2 A44088 56.4 309 1 A49011 56.4 309 2 A3169 56.4 510 2 A4703	48	61.5	220	~	E72464	
60.3 380 2 JC1451 59.0 504 2 AES556 57.7 173 2 AES648 57.7 275 2 C84673 57.7 651 2 A44112 57.7 651 2 A44112 57.1 335 2 S08341 57.1 335 2 S08341 57.1 335 2 A6433 56.4 226 1 S5166 56.4 259 2 A44008 56.4 259 2 A44008 56.4 259 2 A44008 56.4 269 2 A44008 56.4 309 1 A49011 56.4 309 2 A44082 56.4 309 2 A44082 56.4 309 2 A44082 56.4 309 2 A4706 56.4 309 2 A4776 56.4 510 2 S02165 56.4 510 2 S02165	48	61.5	1690	~	T35694	
59.0 333 2 C44423 59.0 504 2 AB5526 57.7 275 2 AB5648 57.7 275 2 C84673 57.7 651 2 A44112 57.1 335 2 A85226 56.4 226 1 A56333 56.4 226 1 A5660 56.4 259 2 A44988 56.4 269 2 A44988 56.4 269 2 A44988 56.4 309 1 A48082 56.4 309 2 A42708 56.4 309 2 A42769 56.4 309 2 A42769 56.4 309 2 A42769 56.4 309 2 A42769 56.4 379 1 A48082 56.4 510 2 A42769 56.4 510 2 A42769	47	60.3	380	~	JC1451	Ca2+/calmodulin-de
59.0 504 2 ABS526 57.7 173 2 AB3648 57.7 275 2 C8648 57.7 627 2 A44112 57.1 335 2 S03341 57.1 730 2 A36333 57.1 730 2 A36226 56.4 226 1 S51660 56.4 259 2 A44098 56.4 269 2 A44098 56.4 269 2 A44098 56.4 309 2 A49011 56.4 309 2 A4908 56.4 309 2 A3169 56.4 309 2 A3169 56.4 510 2 A4708 56.4 309 2 A3169 56.4 309 2 A3169 56.4 510 2 A4703 56.4 510 2 A4703 56.4 510 2 A4703 56.4 510 2 A4703	46	59.0	333	~	C48423	homeotic protein e
57.7 173 2 AB5648 57.7 275 2 C84673 57.7 627 2 A44112 57.7 651 2 A5333 57.7 651 2 A5333 57.1 335 2 A8331 57.1 335 2 A8331 56.4 226 1 S51660 56.4 259 2 A47008 56.4 269 2 A47008 56.4 305 1 A48082 56.4 309 2 A33169 56.4 309 2 A33169 56.4 309 2 A33169 56.4 309 2 A3701 56.4 309 2 A3705 56.4 309 2 A3705 56.4 309 2 A3705 56.4 510 2 A3705 56.4 679 2 S02165 56.4 924 2 A87431	46	59.0	504	7	AE3526	5-carboxymethyl-2-
57.7 275 2 C84673 57.7 627 2 A84112 57.7 651 2 A84313 57.1 335 2 S08341 56.4 226 1 S51660 56.4 232 1 TVFV10 56.4 269 2 A44988 56.4 269 2 A44988 56.4 269 2 A44908 56.4 309 2 A447008 56.4 309 2 A42008 56.4 309 2 A42069 56.4 510 2 A42750 56.4 679 2 S02165 56.4 924 2 F81103 56.4 924 2 A87431	45	57.7	173	7	AB3648	flagellar basal-bo
57.7 627 2 A44112 57.7 651 2 A36333 57.1 335 2 808341 57.1 730 2 A36226 56.4 226 1 S51660 56.4 259 2 A44998 56.4 269 2 A44098 56.4 269 2 A44008 56.4 305 1 A49011 56.4 309 2 A44010 56.4 309 2 A44010 56.4 510 2 A42750 56.4 679 2 802165 56.4 924 2 R81033 56.4 924 2 A87431	45	57.7	275	~	C84673	hypothetical prote
57.7 651 2 A36333 57.1 335 2 A36236 56.4 226 1 S51660 56.4 232 1 TVPV10 56.4 259 2 A44988 56.4 269 2 A47008 56.4 305 1 A49011 56.4 309 2 A39169 56.4 924 2 A87431	45	57.7	627	7	A44112	spidroin 2, dragli
57.1 335 2 \$08341 56.4 226 1 \$54566 56.4 232 1 TVFV10 56.4 26 2 A44988 56.4 26 2 A44008 56.4 286 2 A44008 56.4 286 2 A47008 56.4 305 1 A49011 56.4 309 2 A4700 56.4 510 2 A42750 56.4 520 2 S0165 56.4 924 2 R81033	45	57.7	651	~	A36333	dnaK-type molecula
57.1 730 2 A36226 56.4 226 1 SS1660 56.4 229 1 TVFVI 56.4 269 2 A44988 56.4 269 2 S04673 56.4 305 1 A49011 56.4 309 2 A39169 56.4 379 1 A48082 56.4 510 2 A42750 56.4 679 2 S02165 56.4 924 2 P81033 56.4 924 2 R81433	5.5		335	7	S08341	myristylated alani
4 56.4 226 1 551660 4 56.4 222 1 TVFV10 4 56.4 259 2 A44908 4 56.4 305 2 A47008 4 56.4 309 2 A39169 4 56.4 309 2 A39169 4 56.4 309 2 A39169 4 56.4 309 2 A39169 4 56.4 309 2 B70694 56.4 679 2 S02165 4 56.4 920 2 B70694 56.4 954 2 F87103	4.5		730	~	A36226	collagen alpha 1 c
4 56.4 232 1 TVFV10 4 56.4 259 2 A44988 4 56.4 269 2 A44988 4 56.4 286 2 S04673 4 56.4 305 1 A49011 4 56.4 379 1 A49011 4 56.4 510 2 A42750 4 56.4 924 2 S02165 4 56.4 924 2 R87103 4 56.4 954 2 A87431	44	56.4	226	Н	S51660	histone H1-5 [vali
4 56.4 259 2 A44988 4 56.4 286 2 A44008 4 56.4 305 1 A49011 4 56.4 309 2 A39169 4 56.4 319 2 A39169 4 56.4 510 2 A42750 4 56.4 679 2 S02165 4 56.4 924 2 R87103 4 56.4 954 2 A87431	44	56.4	232	н	TVFV10	transforming prote
4 56.4 269 2 A47008 4 56.4 286 2 S04673 4 56.4 309 2 A39169 4 56.4 309 2 A39169 4 56.4 319 1 A48082 4 56.4 679 2 S02165 4 56.4 920 2 B70694 56.4 954 2 R87103		56.4		7	A44988	transforming prote
4 56.4 286 2 S04673 4 56.4 305 1 A49011 4 56.4 309 2 A39169 4 56.4 379 1 A48082 4 56.4 510 2 A42750 4 56.4 679 2 S02165 4 56.4 924 2 F87103 4 56.4 954 2 A87431	44	56.4	269	7	A47008	transcription acti
4 56.4 305 1 A49011 4 56.4 309 2 A39169 4 56.4 379 1 A48082 4 56.4 510 2 A42750 4 56.4 920 2 B70694 4 56.4 954 2 R87431	44	56.4	286	~	S04673	H+-transporting tw
4 56.4 309 2 A39169 4 56.4 510 2 A42750 4 56.4 679 2 S02165 4 56.4 900 2 B70694 56.4 954 2 F87103	44	56.4	305	-	A49011	c-Crk - chicken
4 56.4 379 1 A48082 4 56.4 510 2 A42750 4 56.4 679 2 S02165 4 56.4 900 2 B70694 5 56.4 924 2 F87103 4 56.4 954 2 A87431	44	56.4	309	~	A39169	myristylated alani
56.4 510 2 A42750 56.4 679 2 S02165 56.4 900 2 B70694 56.4 924 2 F87103 56.4 954 2 A87431	44	56.4	379	٦	A48082	MAP kinase 3 (EC 2
56.4 679 2 SO2165 56.4 900 2 B70694 56.4 924 2 F81103 56.4 954 2 A87431	44	56.4	510	~	A42750	insulinoma-associa
4 56.4 900 2 B70694 4 56.4 924 2 F87103 4 56.4 954 2 A87431	44	56.4	619	~	802165	regulatory protein
4 56.4 924 2 F87103 4 56.4 954 2 A87431	44	56.4		N	B70694	probable infB - My
.4 954 2 A87431		9	N	~	F87103	initiation factor
	44	56.4	954	7	A87431	regulatory protein

adenylate cyclase	ckes-binding proce	hypothetical prote	Hypothetical Prote		DNA-invertase - Rh	hypothetical prote	hypothetical prote	hypothetical prote	jun-D protein - ra	hypothetical prote	Ca2+/calmodulin-de	transcription fact	conserved hypothet	membrane transport
A41350	T13828	T36874	AE3136	G98151	842585	T32525	D70803	B72677	JC4051	855626	S28184	A49642	E82766	T30220
0 0	4 C	1 (1	~	~	7	~	~	N	~	~	~	~	~	N
1134	328	185	189	189	213	260	280	307	341	349	377	420	431	437
56.4	ט ת 4. מ	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1
44 56.4	44 00.4		43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1	43 55.1

ALIGNMENTS

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acclimation protein 2 - barley
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
A;Title: mRNA stability and localisation of the low temperature responsive barley gene
A;Reference number: Z15367; MUID:9729834; PMID:9154983
A;Reference number: Z15367; MUID:9729834; PMID:9154983
A;Accession: T04476
A;Accession: T04476
A;Accession: T04476
A;Accession: T04476
A;Accession: T0476
A;Accession: J0476
A;Accession: J0476
A;Accession: J0476
A;Coss-references: UNIPROT:Q40033; UNIPARC:UPI000099CE5A; EMBL:X97917; NID:g1418969; PA;Gene: D1414.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.1%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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2 GAARASGPGGGAP 14 ઠે

probable oxidoreductase - Streptomyces coelicolor 31 GAARGAGAGGOVP 43 셤

C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
S;Accession: T36115
A;Reference number: 221597
A;Accession: T36115
A;Accession: T36115
A;Residues: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-222 <NUR>
A;Residues: 1-222 <NUR>
A;Cross-references: UNIPROT: Q9X887; UNIPARC: UP100000DB008; EMBL: AL049707; PIDN: CAB41281
A;Experimental source: strain A3(2)

A;Gene: SCOEDB:SCE15.12c C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4); Gaps ö Length 222; 3; Indels Score 50; DB 2; Pred. No. 11; 2; Mismatches Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative

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1 AGAARASGPGGGAP 14

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533 AGAPRVGGPGVQMGGAP 549
                                                                                                                                                                                                                                                   1 AGAARASGPG---GGAP 14
A; Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||| | : ||||: |
181 AGATRVARPGGGSDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1437 GSANGSGPEGSAPR 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.54
Best Local Similarity 64.34
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SCOEDB:SC7C7.16c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-220 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: APE2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
E;Woessner, J.F.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring, Plant Mol. Biol. 26, 947-960, 1994
F;Woessner, Domain conservation in several volvocalean cell wall proteins.
F;Reference number: S50754
F;Reference number: S50754
F;Reference preliminary
F;Reference number: J-1351 ew005>
F;Residues: 1-351 ew005>
F;Residues: 1-351 ew005>
F;Residues: 1-351 ew005>
F;Residues: 1-351 ew005>
F;Residues: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z19373
A;Accession: T21095
A;Accession: T21095
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molicule type: DNA
A;Residues: 1-692 < WILL>
A;Cross-references: UNIPROT:Q19579; UNIPARC:UPI0000079A30; EMBL:Z50110; PIDN:CAA90444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2; Length 351;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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R,Coles, L.
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 AGAPRVGCPGVQMGGAP 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
:|:|||||| | |
180 SGSARASGPSAGRP 193
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295 SGSPRASPPGGGPP 308
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hypothetical protein APE2360 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
B;Accasion: E74464
B;Accasion: E7464
A;Accasion: E72464
A;Accasion: E72464
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A;Molecule type: DNA
A;Residues: 1-1690 cHRA:
A;Cross-references: UNIPROT:086821; UNIPARC:UPI0000DACB6; EMBL:AL031031; PIDN:CAA19862
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9Y9C7; UNIPARC:UPI000005E2F9; DDBJ:AP000064; NID:g5105945;
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A,Map position: X
A,Introns: 111/1, 215/2; 469/3; 552/3
C,Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T35694
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z21587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                   DB 2; Length 692;
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64.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 4; Indels
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                                                                                                                                                                                                   Indels
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                                                                                                                            Query Match 62.2%; Score 48.5; D
Best Local Similarity 64.7%; Pred. No. 45;
Matches 11; Conservative 0; Mismatches
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Ribelyecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.Delyecchio, V.G.; Kapatral, V.; Relkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q8YDP0; UNIPARC:UP10000058376; GB:AE008918; PIDN:AAL53376.1
A,Experimental source: strain 16M
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C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                           5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (BC 1.2.1.-) [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
                                                                                                                                                                                                                                                                                                                                                                 C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3526
                                                                   Gaps
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      Length 333;
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                                                             4; Indels
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Pred. No. 39;
0; Mismatches
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                            Pred. No. 51;
1; Mismatches
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      Score 46;
Pred. No.
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Pred. No.
59.0%;
64.3%;
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66.7%;
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                                                                                                                      1 AGAARASGPGGGAP 14
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                                                             Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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Query Match
Best Local Similarity
Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-504 <KUR>
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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A,Map position: II
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A; Cross-references: UNIPARC: UPI00001707CE; GB: U12008; GB: S59509; NID: G515498; PIDN: AAA20
C; Superfamaily: kinase-related transforming protein; protein kinase homology
C; Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F; 41-331/Domain: protein kinase homology ckn.
F; 49-57/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:956626; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 14-380 «BOU»
A; Crosd-verferences: 10.1800
A; Crosd-verferences: UNIPARC: UPI0000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID:
R; Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
Biochemistry 30, 278-286, 1991
A; Title: Purification and properties of extracellular signal-regulated kinase 1, an insu
A; Reference number: A37140; MUID:91105092; PMID:1846291
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R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
A;Title: A;Title: Asquence comparison of the mouse, human, and chicken engrailed gene A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Boulton, T.G.; Yancopoulos, G.D.; Gregory, J.S.; Slaughter, C.; Moomaw, C.; Hsu, J.; Science 249, 64-67, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 43-64;167-178, XX', 180-183, XX', 185 < BO2>
A; Residues: 43-64;167-178, XX', 180-183, XX', 185 < BO2>
A; Cross-references: UNIPARC: UPTO00017558F; UNIPARC: UPTO000175590
R; De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA, Cell Biol. 10, S05-514, 1991
A; Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
A; Reference number: A40466; MUID: 91369479; PMID: 1716439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in A;Reference number: A35061; MUID:90312137; PMID:2164259
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                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-5ep-1993 #sequence revision 30-5ep-1993 #text_change 09-Jul-2004
C;Accession: JC1451; A35061; A37140; A40466; S24947
R;Marquardt, B.; Stabel, S.
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
                      Ca2+/calmodulin-dependent protein kinase (BC 2.7.1.123) - rat
N/Alternate_names: BRK1-MAP kinase; extracellular signal-regulated kinase
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;245-301/Domain: homeobox homology <HOX>
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                                                                                                                                                                                             A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase. A;Reference number: JC1451; MUID:93013050; PMID:1327976
A;Accession: JC1451;
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Best Local Similarity 66.7
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A;Title: Molecular and developmental characterization of the heat shock cognate 4 gene c. A,Receence number: A36333; MUID:90258915; PMID:2111451
A,Raceausion: A36333; MUID:90258915; PMID:2111451
A,Raceausion: A36333; MUID:90258915; PMID:2111451
A,Reseiuus preliminary
A,Molecule type: DNA
A,Reseiuus: 1-651 < PER>
A,Reseiuus: 1-651 < PER>
A,Genetics: WIPROT:P11147; UNIPARC:UPI000016BC3E; GB:M36114; NID:g157663; PIDN
A,Genetics: FlyBase:H670-4
A,Genetics: RiyBase:RBgn0001219
C,Geneticn: A,Geneticn: Involved in protein folding and assembling/disassembling of protein compll
C,Superfamily: bcr protein
C,Superfamily: bcr protein
C,Superfamily: molecular chaperone; nucleus
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N;Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; S29270; A46098; PS0338
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
A;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
A;Title: Nuclectide sequence of a CDNA for the bovine myristoylated alanine-rich C kinasi A;Reference number: S08341; MUID:89282412; PMID:2734111
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: This cstu-
A;Molecule type: Lass cstu-
A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PID]
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
R;Stumpo, D.J.; Graff, J.M.; Albert, M.A.; Greengard, P.; Blackshear, P.J.
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
A;Reference number: A32904; MUID:89264553; PMID:2726763
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A;Status: nucleic acid sequence not shown
A;Acsession: A32204
A;Accession: Salates: nucleic acid sequence not shown
A;Residues: 1-98, Q, 100-335 <ST2>
A;Residues: 1-98, Q, 100-335 <ST2>
A;Cross-references: UNIPARC:UP1000017750A; GB:M24638; GB:M23738
B;Herget, T.; Brooks, S;F; Brood, S;; Rozengurt, E.
Bur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein
A;Reference number: S29267; MUID:93011168; PMID:1396720
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A;Residues: 191-253, SEE', 257-279, 283-292,'V', 294,'PEQE', 299,'A',300,'A',302-313,'A',315
A;Cross-references: UNIPARC:UP1000017750B
A;Cross-references: UNIPARC:UP1000017750B
B;Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
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A,Moseidues 2-11 - WANN.
A,Residues 2-11 - WANN.
A,Gross-references: UNIPARC:UDI000017750C
R,Mizutani, A.; Tokumitsu, H.; Hidaka, H.
R,Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with A,Reference number: PS0338; MUID:92171958; PMID:1540183
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A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'B',111-123;156-160;165-171;196-215;2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Isolation of the non-myristoylated form of a major substrate of protein kinase A,Reference number: A46098; MUID:93216617; PMID:8463217
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Pred. No. 1.2e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.7%;
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Best Local Similarity 64.3
Matches 9; Conservative
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NyAlternate names: silk fibroin, dragline
C;Species: Nephila clavipes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A44112; S27824
E;Hinman, M.B.; Lewis, R.V.
J. Biol. Chem. 267, 19320-19324, 1992
A;Fitle: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Faccession: A44112; MulD:92406876; PMID:1527052
A;Accession: A44112; MulD:92406876; PMID:1527052
A;Accession: A44112
A;Status: preliminary
A;Residues: 1-627 - AIN>
A;Coss-references: UNIPROT:P46804; UNIPARC:UPIO000135DC6; GB:M92913; NID:gl59713; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIP:113893)
B;Hinman, M.B.; Lewis R.V.
submitted to the EMBL Data Library, May 1992
A;Decenter under EMBL Data Library, May 1992
A;Decenter Data Library, May 1992
A;Dec
                                                                                                                                                                         C'Accession: C84673
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koul, H.; Moffart, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Resession: C84673
A;Status: preliminary
A;Residues: 1-275 <STO>
A;Cross-references: UNIPROT:Q9ZQH2; UNIPARC:UP1000000C26F; GB:AE002093; NID:g4314389; PIC;Genetics:
C;Genetics:
A;Map position: 2
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N;Alternate names: heat shock cognate protein 70
C;Species: Drosophila melanogaster
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 31-Dec-2004
C;Accession: A3633
R;Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A.Mol. Cell. Biol. 10, 3232-3238, 1990
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                                                      hypothetical protein At2g27470 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C jate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: C84673
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Pred. No. 1.2e+02;
1; Mismatches 4; Indels
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A)Accession: S27824
A)Molecule type: mRNA
A)Residues: 19-627
A)Cross-references: UNIPARC:UP1000017BE0B; EMBL:M92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pred. No.
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76.98;
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity
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A.Experimental source: brain
A.Note: this sequence is identical with that of myristcylated alanine-rich C-kinase subs
C.Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C.Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
C.Genetics:
A.Introns: 34/3
A.Introns: 34/3
A.Introns: 34/3
A.Introns: 34/3
A.Introns actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;188,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 13, 2006, 19:16:10 Job time : 19.8235 secs
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Title: Perfect score:

Seguence:

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Scoring table:

Searched:

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toxoplasma
homo sapien
homo sapien
chlamydomon
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mus musculu
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Name-CTAGIB; Synonyms-CTAG, CTAGI;
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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NUCLECAIDE SEQUENCE.
NUCLECAIDE SEQUENCE.
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S., Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY
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06h6a6
086pil
096dh8
069h7b9
09h7p9
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061288
065288
0692k9
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Pred. No. 0.012;
; Mismatches 0; Indels
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Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ275978; CAB76945.1; -; MRNA.
Hypothetical protein.
NON_TER
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Last annotation update)
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               Q86PII_TOXGO
Q96D18_HUMAN
Q6DHV6_HUMAN
Q9H7P9_HUMAN
Q9M4X9_CHLRE
NLGRN2_HUMAN
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                                                                                                                    QSF288 MOUSE
Q69ZK9 MOUSE
Q94LU4 ORYSA
Q9DCH0 MOUSE
                                                                                                                                                                                  PACA CHICK
Q63HT9 BURPS
                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment)
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15-DEC-1998 (Rel. 37, Last seq
10-MAY-2005 (Rel. 47, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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Best Local Similarity
 Homo.
NCBI_TaxID=9606;
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 RESULT 1
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CTG1B HUMAN
ID CTG1B H
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97.196 Million cell updates/sec
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                                                                                                    March 13, 2006, 18:53:23 ; Search time 108.882 Seconds
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971by

972by

97
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                         2166443 seqs, 705528306 residues
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Q7T5D9_CHV1
Q7T591_CHV1
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Q96S27_HUMAN
Q67PJ0_SYMTH
Q689J5_QRYSA
Q7QEKS_ANOGA
Q4NQS2_9DELT
Q9GRA8_GRYBI
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07LBY4 HUMAN

CTAG2 HUMAN

CT086 HUMAN

09L680 ORYSA

091LD1 ORYSA

063QT8 BURPS

062H22 BURPS
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9ADEN
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Q75IL4 ORYSA
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                                                                       - protein search, using sw model
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O96BU2
O9X887
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Gapop 10.0 , Gapext 0.5
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78
1 AGAARASGPGGGAPR 15
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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786
3328
3326
367
405
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Score

Result Š. a 35

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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T.; and gene with tumor specificity."; ILAGE-1, a new gene with tumor specificity."; Int. J. Cancer 76:303-908(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS GLA-6; GLA-89 AND ARG-138.
                 "Multiple pathogenic and benign genomic rearrangements occur at
kb duplication involving the NEMO and LAGE2 genes.";
Hum. Mol. Genet. 10:2557-2567(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set
line- and tumor-pecific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ©TAG2 HUMAN STANDARD; PRT; 210 AA. 075639; 075639; 091089; 094479; 30.-MAY-2000 (Rel. 39, Created) 30.-MAY-2000 (Rel. 39, Last sequence update) 10.-MAY-2005 (Rel. 47, Last annotation update) Cancer/testis antiqen 2 (LAGE-1 protein) (ESO-2 protein). Name=CTAG2; Synonyms=ESO2, LAGE1;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                           M.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                     Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF277315; AAL27014.1; -; Genomic_DNA.
EMBL, AJ275977; CAB76943.1; -; Genomic_DNA.
EMBL, AF277315; AAL27013.1; -; Genomic_DNA.
SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B)
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MEDLINE=98289662; PubMed=9626360;
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Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
Galgoczy P., Platzer
Submitted (MAR-2003)
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Nelson D.L.;
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                                                                                                                                                                                                                                                  Platzer M
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                                                                                                                                                 Platzer
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Matches
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                               MEDLINE=98430682; PubMed=9759882; Wang R.-F., Johnston S.L., Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosemberg S.A.; Pareast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames."; J. Immunol. 161:3596-3606(1998).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
                                                                                                                Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano de Plaen B., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:902-908(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 78; DB 1; Length 180;
Pred. No. 0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             variety of cancers. Detected in uterine myometrium.
-!- SIMILARITY: Belongs to the CTAG family.
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Gly-rich.
B122C5C2C8BE1569 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
uomo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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TRANSMEM 156 172
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobliyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Notlaton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Schnerch A., Schein J.R., Vonge S.J.M., Marra M.A.,
F. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBD outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
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LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
                                                                                                                                                                                                                                                                                                                                                                                                             and mouse CDMA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=LAGS-1B; Synonyms=LAGS-1L;
Isold=075638-1; Sequence=Displayed;
Name=LAGS-1A; Synonyms=LAGS-1S;
Isold=075638-1; Sequence=VSP_004301;
-!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and head and neck cancers.
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8BE0EE00AE55E8BE CRC64;
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/FTId=VAR_007856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
EMBL; AJ223093; CAA1116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
EMBL; AJ012834; CAA10194.1; -; mRNA.
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                                       TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPBIAS
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MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

Radiey J., Barlow K.P., Barles K.N., Beard L.M., Beard D.M.,

Radiey J., Barlow K.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

Radiey D., Bird C.P. Blakey S.E., Bridgeman A.M., Brown A.J.,

Radiey J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

Rolegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Blington A.G., Frankland J.A., Fraser A., French L., Howden P.J.,

Ammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

Ray M.P., Kimberley A.M., King A., Krights A., Laird G.K., Lawlor S.,

Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachle L.J., McLay K., McMurray A.A.,

Milne S.A., Miscry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Allimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rames D.W., Thorpe A.,

Skuce C.D., Smith M.L., Socht C.E., Schra H.K., Showheen R., Sime S.,

Skuce C.D., Smith M.L., Socht C.E., Schra H.K., Showheen R., Sine S.,

Skuce C.D., Smith M.L., Socht C.E., Schra H.K., Showheen R., Sine S.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Racey A., Tromans A.C., Vaudin M., Wallis J.M.,

Milining L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beltkin B. A.,

Milling D., Wray P.W., Hubbard T., Durbin R.W., Bentley D.R., Beck S.,

M. Holling R. M. Hubbard T., Durbin R.W., Bentley D.R., Beck S.,

Recentles A. M. Hubbard T., Durbin R.M., Bentley B.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bilinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
-!- SIMILARITY: Contains 2 ANK repeats.
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00248; ANK; 2.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS500299; UBIQUITIN 1; FALSE_NEG.
PROSITE; PS50053; UBIQUITIN 2; 1.
ANK repeat; Hypothetical protein; Polymorphism; Repeat.
                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                          337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P42771; 2A5E.
Ensembl; ENSG00000124227; Homo sapiens.
                                                                                                                                                          PRT;
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InterPro; IPR002110; ANK.
InterPro; IPR00626; Ubiquitin.
Pfam; PF00023; Ank; 2.
PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                                          Hypothetical protein C20orf86.
                          STANDARD;
                                                                                                                                                                                                                                                                                                   Name=C20orf86;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                          CT086_HUMAN
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                                                                                                                                                                                  Q9BZ19;
                                                                                                                                         CT086_HUMAN
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Gaps

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Query Match

89.7%; Score 70; DB 1; Length 210;
Best Local Similarity 93.3%; Pred. No. 0.19;
Matches 14; Conservative 0; Mismatches 1; Indels

867 AA

PRT;

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Q94LD1 ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                          [1]
NUCLEOTIDE SEQUENCE.
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les 10; Conserv
                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
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                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Zismann V., Haiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Eterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; ACO92388; AAM22719.1; -; Genomic_DNA. EMBL, AAE53592.1; -; Genomic_DNA. Gramene; QBL680; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 559;
                                                                                                                                                               Length 337;
                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 559 ÅA; 58950 MW; A5B4492C2D3F94FA CRC64;
                                                                                                                   337 AA; 36714 MW; EC8BA4AD414756CB CRC64;
                                                                    R -> C (in dbSNP:584855).
/FTId=VAR_014400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OSJNBa0011L09.12.
ORFNames=OSJNBa0011L09.12;
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66.7%; Pred. No. 42;
cive 1; Mismatches
                                                                                                                                                                  DB 1;
Ubiquitin-like.
ANK 1.
ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                              559 AA.
                                                                                                                                                             70.5%; Score 55; DB 73.3%; Pred. No. 27; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro.; 1PR007228; DUF390.
InterPro; IPR007321; Transposase_28.
Ffam; PF04094; DUF390; 2.
Pfam; PF04195; Transposase_28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                       Science 300:1566-1569(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                          QBL680_ORYSA PRELIMINARY;
                                                                                                                                                                                   Local Similarity 73.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
  88
211
244
287
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                                                                                                                   SEQUENCE
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                                                                                                                                                               Query Match
                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                   ORYSA
                      REPEAT
                                                 REPEAT
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  FTFFF
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Q94LD1 ORYSA

RESULT 7

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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAINERS643;

Pubmed=1537794; DOI=10.1073/pnas.0403302101;

Rubmed=15377794; DOI=10.1073/pnas.0403302101;

Rudden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., And R. Cokersoach I., Chrossett B., Davis P., DeShazer D., Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D., Chillingworth T., Fraser A., Hauser H., Holroyd S., Jagels K., Aseltwell T., Fraser A., Moule S., Price C., Quail M.A., Aseltwell R.E., Maddison M., Moule S., Price C., Quail M.A., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Shmondic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei., The causative agent of melioidosis, Burkholderia pseudomallei., Forc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                    Oryza sativa (Rice).
Skaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                   White O., Fraser C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buell R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2001) to the EMBL; ACO84404; AAK50601.1; -; Genomic_DNA. Gramene; Q94LD1; -. InterPro; IPR007228; DUF390. InterPro; IPR007321; Transposase_28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative DNA polymerase III.
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.5%; Score 55; DB 66.7%; Pred. No. 63; ive 1; Mismatches
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque
01-MR-2004 (TrEMBLrel. 26, Last annot
Hypothetical protein OSJNBa0026A15.11.
Name=OSJNBa0026A15.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGAARASGPGGGAPR 15
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Q63QT8;
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Matches

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RESULT 9

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                      Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; "Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higgs D.R.; "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                      dehalogenans 2CP-C.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339; Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                    Anaeromyxobacter delalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                           STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 2; Length 895;
Pred. No. 88;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 53; DB 2; Length 321; 66.7%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                  Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAHD0100013; EAL79351.1; -; Genomic DNA.
SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BDB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
Ensembl; ENSG0000167933; Homo sapiens.
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                                                                                                                                                STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-PGF);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%;
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Best Local Similarity 73.33,
Best Local 11; Conservative
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3 SAARRAGPGGGAAR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                 NCBI_TaxID=290397;
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PubMed=1537793; DOI=10.1073/pnae.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Reldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J., Markin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M.;

"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. US.A. 101:14246-14251(2004).

EMBL. CP000010; AAU49707.1; -; Genomic_DNA.
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerae III, delta subunit (EC 2.7.7.7).
Name-holA; OrderediocusNames-BMA2451;
Burkholderia mallei (Pseudomonnas mallei).
Bacteria; Proteobacteria; Becaproteobacteria; Burkholderiacea; Burkholderia.
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GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA. GO; GO:0006260; P:DNA replication; IEA. InterPro; IPR010372; DNA pol3 delta. InterPro; IPR05790; DNA pol1II delta. Pfam; PF06144; DNA pol3 delta; I. TIGRFAMS; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; BMA2451; ...

GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR010372; DNA pol3 delta.

InterPro; IPR005790; DNA pol1II delta.

Pfam; PP06144; DNA pol3 delta; I.

TIGRFAMS; TIGR01128; holA; 1.

Complete proteome; Nucleotidyltransferase; Transferase.

SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                   Length 362;
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                                                                                                                                         362 AA; 38726 MW; DSFF3DE783D41E41 CRC64;
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Last annotation update)
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                            362 AA
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Pred. No.
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83.3%;
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83.3%;
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1D O4NUK4 9DELT PRELIMINARY;
AC QANUK4;
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31,
DE LigA.
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Q62H22;
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348 ARAAGPGGDAPR 359
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Best Local Similarity 83.3
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                                                                                                                         Complete proteome. SEQUENCE 362 AA;
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ses 10; Conserv
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644 AA;
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Chow T.-Y., Haing Y.-I.C., Chen H.-C., Chen S.-K., Chen T.-R.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Cheng C.-H., Chung C.-H., Hans S.-Y., Lin S.-Y.,
Haiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
Li Y.-F., Lin Sr-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa BAC OSJNBb0012621 genomic sequence.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AC13541; AAU10755.1; -; Genomic_DNA.
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last amotation update)
Hypothetical protein OSJNBb0012621.2.
Name-OSJNBb0012621.2;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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GO; GO:0004057; F:arginyltransferase activity; IEA.
GO; GO:0016598; P:protein arginylation; IEA.
GO; GO:0042176; P:requlation of protein catabolism; IEA.
InterPro; IPR007472; ATE_C.
InterPro; IPR007471; ATE_C.
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                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                  Symbiobacterium thermophilum
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Q68812-QRYSA PRELIMINARY;
AC Q68815;
                                                                                 Q67PJO_SYMTH PRELIMINARY;
Q67PJO;
                                                                                                                                                                                                                                                                                     OrderedLocusNames=STH1418
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                                                                                                                                                                                                                                                    Prephenate dehydrogenase.
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Neoptera; Bndopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelimae; Anopheles.
NCBI_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PBST;
The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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R GO; GO:0008005 C: integral to membrane; IEA.

R GO; GO:0008515; F:protein binding; IEA.

R GO; GO:0007160; P:cell-matrix adhesion; IEA.

R GO; GO:0007250; P:integrin-mediated signaling pathway; IEA.

R HOLESPEO; IPRO0041; Integrin_alpha.

R Ffam; PF01839; FG-GAP; 3.

R PRINTS; PR01185; INTEGRINA.

R SMART; SM0199; Integrin_alpha; 1.

R SMART; SM0199; Integrin_alpha; 6.

Cell_adhesion; Integrin; Transmembrane.
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                                                Length 644;
                                                                                                1; Indels
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SEQUENCE 1379 AA, 149836 MW; 2D6945E834F3DD75 CRC64;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
72444 MW; DDB97FC0C40C23F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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71.4%; Pred. No. 1.7e+02;
iive 0; Mismatches 4;
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                                             Score 53; DB 2
Pred. No. 88;
1; Mismatches
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01-MAR-2004 (TrEMBLrel. 26, Li
01-MAR-2004 (TrEMBLrel. 26, Li
01-MAR-2000 (TrEMBLrel. 26, Li
ENSANGPO00000447 (Fragment)
ORFNames=ENSANGGO000003703;
                                                67.9%;
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Q4NQS2;
13-SEP-2005 (TEMBLEEL: 31,
13-SEP-2005 (TEMBLEEL: 31,
13-SEP-2005 (TEMBLEEL: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae str. PEST
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                                                                                                10; Conservative
                                                                                                                                              1 AGAARASGPGGG 12
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ORFNames=AdehDRAFT_11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                             Query Match
Best Local Similarity
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STRAIN=2CP-C;
STRAIN=2CP-C;
Copeland A., Lucae S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               7;
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
                                                                                                                                                                                                                                                                         Query Match 67.3%; Score 52.5; DB 2; Length 924; Best Local Similarity 59.1%; Pred. No. 1.46+02; Matches 13; Conservative 1; Mismatches 1; Indels 7
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Search completed: March 13, 2006, 19:14:26 Job time: 111.882 secs

1 AGAARASGPG-----GGAPR 15

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21865, A 20125, A 2, Appli 3, Appli 25611, A 4, Appli 4, Appli 26, Appli

Sequence 3 Sequence 2 Sequence 4 Sequence 4

Sequence Sequence Sequence

Sequence 1 Sequence 2 Sequence 5 Sequence 5 Sequence 2 Sequence 2

Sequence Sequence

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100.0%; Score 78; DB 1; Length 180; 100.0%; Pred. No. 0.01; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
US-09-252-991A-20577

US-09-252-991A-31279

US-10-104-047-3295

US-09-252-991A-19800

US-09-252-991A-20512

US-09-417-197-57

US-09-417-197-57

US-09-252-991A-20165

US-09-252-991A-20165

US-09-252-991A-20125

US-09-464-377-3

US-09-464-377-3

US-08-464-377-3

US-08-938-201A-4

US-08-589-619-4

US-08-589-619-4

US-08-209-147-37

US-08-209-147-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                           JS-08-317-844B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08791495
Patent No. 5811519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGAARASGPGGGAPR 15
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Sequence 15, Appl
Sequence 30, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 17335, A
Sequence 17345, A
Sequence 17249, A
Sequence 17249, A
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Sequence 10, Appl
Sequence 7, Appli
Sequence 3, Appli
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Sequence 117, App
Sequence 117, App
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Sequence 23998, 1
Sequence 31759, 1
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                                                                                                                                 March 13, 2006, 19:14:49; Search time 27.8824 Seconds (without alignments) 44.477 Million cell updates/sec
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Sequence 25, 7
Sequence 15, 7
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Sequence 8,
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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-937-263B-8
US-09-392-714-25
US-09-341-825-8
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US-09-252-991A-17345
US-09-252-991A-17249
US-09-252-991A-17249
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US-09-252-991A-3326
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US-09-325-991A-3326
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US-09-252-991A-31759
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                                                                                                                                                                                                                                                                                                                                                       572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                  Sequence 8, Application US/08937263B

Patent No. 6274145

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GLEC, Ali; Old, Lloyd J., Jager, Elke;

APPLICANT: GLEC, Ali; Old, Lloyd J., Jager, Elke;

APPLICANT: Alexander, Kunth; Drijfhout, Jan W.

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, TITLE OF INVENTION: INSERT, AND USES THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSES: Fulbright & Jaworski, L.L.P.

STREET: 66 FIfth Avenue

CITY: New York City

COUNTRY: USA

COUNTRY: Hew York

COUNTRY: Hew York

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

OPERATING SYSTEM: PC-DOS

SOFTWARE: Worderfect

COMPUTER: Morderfect

SOFTWARE: Worderfect

COMPUTER: Worderfect

COMPU
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APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
ATTLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09751798; Sequence 8, Application US/09751798; Patent No. 6525177; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGAARASGPGGGAPR 15
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 78; DB 2; Length 180;
100.0%; Pred. No. 0.01;
tive 0; Mismatches 0; Indels
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US-09-392-714-25

US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 6686147

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.

APPLICANT: Ganalan, Matthew J.

APPLICANT: Gure, Ali O.

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Cancer Associated Antigens and Uses

TITLE OF INVENTION: Cancer Associated Antigens and Uses

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: UNMERR: US/09/392,714A

CURRENT FILING DATE: 1999-09

EARLIER PILING DATE: 1999-009

EARLIER PILING DATE: 1999-009

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

LEWITH: 180
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ZUCOMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
AMDIUM TYPE: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                            COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILLING DATE: 09/062,422
FILLING DATE: 09/062,422
FILLING DATE: 05-06-F 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525,77man D.
REGISTRATION NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG ID NO: 8:
TELEFAX: (212) 752-5958
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-392-714-25
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  <151> 1998-01-27
                                                                                                                                                                                       100.0%; Score 78; DB 2; Length 180; 100.0%; Pred. No. 0.01; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78; DB 2; Length 180; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charlee
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STOPHESSEE: Wolf C...
STOPHESSEE: Wolf C...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Old, Lioyd J.
APPLICANT: Stockert, Elieabeth
APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REPERRENCE: L046.1/7105.1/207
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                 NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
APPLICATION NUMBER: PCT/US98/01445
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 30, Application US/09849602; Patent No. 6794501
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Patent No. 5811519
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Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Scanlan, Matthew J.
                                                                                                                                                                                                                                                                           1 AGAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                          48 AGAARASGPGGGAPR 62
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MEDIUM TYPE: Floppy
                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                         Best Local Similarity
Matches 15; Conserv
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                                                                                                                                               US-09-341-829A-9
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                                                                                                                                                                                         Query Match
                                                                                    LENGTH:
PRIOR
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                                                                                               APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6723832man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 10,946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 2; Length 180;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                      ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: ISM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPREBRUCE: LO461/706
CURRENT APPLICATION NUMBER: U$/09/341,829A
CURRENT FILING DATE: 1999-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/062,422

FILING DATE: APril 17, 1998

APPLICATION NUMBER: 08/937,263

FILING DATE: SEPTEMBER: 15, 1997

APPLICATION NUMBER: US 08/725,182

FILING DATE: OCCODER 3, 1996
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
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TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
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                                 Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGAARASGPGGGAPR 15
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: USA
                 US-09-165-546D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-341-829A-9
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Score 70; DB 1; Length 210; Pred. No. 0.11;
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
  Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      L0461/7005
                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-720-241
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                       600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.7%;
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Best Local Similarity 93.3<sup>3</sup>
----hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                       STREET: 600 # CITY: Boston
                                                                                COUNTRY: USA
ZIP: 02210
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-341-829A-5
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LENGTH: 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09341829A

Patent No. 6794131
GENERAL INFORMATION:
APPLICANT: Lucth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPRENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: PCT/US98/01445
PRIOR APPLICATION NUMBER: PCT/US98/01445
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NOS: 14
SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                   cwery match
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

89.7%; Score 70; DB 2; Length 180;
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 1; Indels
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Patent No. 5011519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smer, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                          L0461/7005
APPLICATION NUMBER: US/08/791,495
                FILING DATE:
CLASSIFICATION: 435
ATTOWNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461).
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-720-3500
TELEFAX: 617-720-341
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-341-829A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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1; Indels

ô Gaps . 0 <151> 1997-01-27 <151> 1998-01-27 Sequence 5, Application US/09341829A

Sequence 5, Application US/09341829A

Patent No. 6794131

GENERAL INFORMATION:
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A

CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US/09/341,495
PRIOR APPLICATION NUMBER: PCT/US/98/01445

SOUTHWARE: FASTSEQ for Windows Version 3.0 Query Match 89.7%; Score 70; DB 2; Length 210; Best Local Similarity 93.3%; Pred. No. 0.11; Matches 14; Conservative 0; Mismatches 1; Indels

Gaps

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3; Indels

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Sequence 13196, Application US/09902540

Factor No. 683340

Factor No. 68340

Factor No. 6840

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Pred. No. 26;
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66.7%; Pred. No. 54;
iive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
       PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17249
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 13, 2006, 19:18:50 Job time : 27.8824 secs
                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249
                                                                                                                                                                                                                                                                                                                                                                                     64.1%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGAARASGPGGGAPR 15
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72 AGTAPAAGPGATAPR 86
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Best Local Similarity 66.7*
These 10; Conservative
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SEQ ID NO 13196
LENGTH: 366
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠.
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                                              Sequence...

Sequence...

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGAINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBNCE: 107196.136

CURRENT PILLIG DATE: 1999-02-18

PRIOR PILLIG DATE: 1999-02-18

PRIOR PILLIG DATE: 1998-02-18

PRIOR PILLIG DATE: 1998-02-18

PRIOR FILLIG DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 456
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24923
LENGTH: 210
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Whenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION; NUMBER: US 60/074,788
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71.8%; Score 56; DB 2; Length 210;
Best Local Similarity 73.3%; Pred. No. 6;
Matches 11; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.4%; Score 58; DB 3
Best Local Similarity 73.3%; Pred. No. 6.8;
Matches 11; Conservative 1; Mismatches
                                      Sequence 17335, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-24923
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US-09-252-991A-17335
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Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Scoring table:

Searched:

Database

Result

Perfect score: Sequence:

Run on:

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 496, App

Sequence

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APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REPRENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin Version 3.2
SEQ ID NO 1404
LENGTH: 30
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100.0%; Score 78; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels
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US-10-295-027-388
US-10-188-832-141
US-10-117-937-75
US-10-117-937-75
US-10-205-734-834
US-10-205-734-834
US-10-657-022-75
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US-11-067-159-75
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US-10-157-031-88
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Sequence 202, Application US/10482029
Fublication No. US20050037445A1
GENERAL INFORMATION:
APPLICANT: ODIN medical A/S
TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 202
LENGTH: 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: NYSOla segment
US-10-296-734-1404
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210
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210
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                           JS-10-296-734-1404
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      RESULT 2
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Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
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Seguence 202, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      March 13, 2006, 19:51:56; Search time 90.7059 Seconds (without alignments) 69.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5024,
Sequence 74, A
Sequence 74, A
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Sequence 3, M
Sequence 386, Sequence 832, Sequence 139, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 9, M
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Sequence 27
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Sequence 8,
Sequence 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA Main:*

cgn2_6/ptodata/1/pubpāa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-482-202
US-09-849-602-30
US-10-027-655-71
US-10-207-655-71
US-10-207-655-71
US-10-206-066-3
US-10-10-107-937-74
US-10-10-107-937-74
US-10-296-073-139
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US-10-296-073-139
US-10-108-93-139
US-10-751-08-15
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US-10-877-273-19
US-10-895-523-3
US-10-895-523-3
US-10-895-523-3
US-10-895-523-3
US-10-875-508-3
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US-09-821-883-27
US-11-144-912-27
US-10-296-734-1454
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                 1 AGAARASGPGGGAPR 15
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Maximum DB seq length: 200000000
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Match Length
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US-10-023-182-8
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                                                                                                                                                                                                                                         Sequence 8, Application US/09751798

Patent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert Elisabeth, Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bland to NY-ESO-1 Cancer;
TITLE OF INVENTION: Truncated Proteins, Uses Thereof;
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
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0
Query Match 100.0%; Score 78; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 0.068; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 3; Length 180;
Pred. No. 0.068;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILLING DATE:
PRIOR APPLICATION NUMBER: 08/725,182
FILLING DATE: 08/725,182
TELEPHONE: 100.0520020010321Alman D.
TELEPHONE: 100.05466.3
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5958
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fulbright & Jaworski, L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYGTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
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Best Local Similarity 100.0%;

Matches 15; Conservative 0.
                                                                                          1 AGAARASGPGGGAPR 15
                                                                                                                         48 AGAARASGPGGGAPR 62
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-751-798-8
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Sequence 30, Application US/09849602 Publication No. US20030165834A1 GENERAL INFORMATION APPLICANT: Scanlan, Matthew J. APPLICANT: Old, Lloyd J.

RESULT 4 US-09-849-602-30

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Gaps
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Sequence 8, Application US/10023182
Publication No. US20020164665A1
GENERAL INPORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-teeng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 78; DB 3; Length 180; 100.0%; Pred. No. 0.068; tive 0; Mismatches 0; Indels
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ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. US20020164665Alman D. REGISTRATION WNDBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
APPLICANT: Stockert, Elisabeth
TITLE OF INVENTION: Colon Cancer Antigen Panel
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER: PS SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: cubknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                            TYPE: PRT CORGANISM: Homo sapiens US-09-849-602-30
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Gaps
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                         APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PERSENTING CELLS
FILE REFERENCE: CTLIMM.21CPIC
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT PILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 78; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0.
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Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: SIMARD, John, J.L.
APPLICANT: BIANDD, David, C.
APPLICANT: LID, Liping
APPLICANT: LIU, Liping
APPLICANT: SIMARD, JOHN, J.L.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
CURRENT APPLICATION NUMBER: US/10/117, 937
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 180
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ORGANISM: Homo mapienm
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| Sequence 14, Application US/2030175250A1
| Sequence 14, Application Word US20030175250A1
| Sequence 14, Application Word US20030175250A1
| Sequence 14, Application Word US20030175250A1
| APPLICANT: USGRATION: Secha | APPLICANT: Glidatic, Sacha | APPLICANT: Glidatic, Sacha | APPLICANT: Glidatic, Sacha | FILE REFERENCE: LUD 5726.1 Clp | CURRENT APPLICATION NUMBER: US/10/364,614
| CURRENT APPLICATION NUMBER: US/10/364,614
| PRIOR APPLICATION NUMBER: US 60/355,828 | PRIOR PLING DATE: 2002-02-13 | NUMBER OF SEQ ID NOS: 17 | SOFTWARE: Patentin Version 3.2
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Sequence 71, Application US/10207655
Publication No. US20030118592A1
Sequence 71, Application WS/10207655
Subjection No. US20030118592A1
SERVERAL INFORMATION:
APPLICANT: Hadbetter, Jeffrey A.
APPLICANT: Hadbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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ch 100.0%; Score 78; DB 4; Length 180; I Similarity 100.0%; Pred. No. 0.068; 15; Conservative 0; Mismatches 0; Indels
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; Publication No. US20030215425A1
                                                                                                              1 AGAARASGPGGGAPR 15
                                                                                                                                                   48 AGAARASGPGGGAPR 62
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-207-655-71
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US-10-364-614-14
                         Best Local Similarity
Matches 15; Conserva
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LENGTH: 180
TYPE: PRT
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LENGTH: 180
  Query Match
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                                                                                                                                                                                                                                                                                                          APPLICANT: Hevez, perer A.
APPLICANT: Hower, parid H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Wateron, Susan R.
APPLICANT: Wateron, Susan R.
APPLICANT: Wateron, Susan R.
APPLICANT: Wateron, Susan R.
APPLICANT: ESS Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
FITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-01250003
CURRENT APPLICATION NUMBER: US /10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2002-01-10
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Publication No. US20040054137A1

GENERAL INFORMATION:
APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR PILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 832
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100.0%; Pred. No. 0.068;
tive 0; Mismatches 0; Indels
Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                     APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAARASGPGGGAPR 15
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-295-027-386
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US-10-296-734-832
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GEREKAL INFUGANT:

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Bas Biotechnology, Inc.

ITILE OF INVENTION: Methods of Diagnosis of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: and Methods of Screening for Modulators of Bladder

ITILE OF INVENTION: Cancer

ITILE REFERENCE: 018501-0023300S

CURRENT APPLICATION NUMBER: US 60/310,099

PRIOR PAPLICATION NUMBER: US 60/310,099

PRIOR PILING DATE: 2001-01-03

PRIOR PAPLICATION NUMBER: US 60/343,705

PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR SEQ ID NOS: 207

SOFTWARE: PatentIn Ver. 2.1

**SEQ ID NO 139
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Publication No. US20040132088A1
Publication No. US2004013208BA1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Qiu, Zhiyong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.02221
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
FRIOR FILING DATE: 2002-11-07
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TYPE: PRT
GOGANISM: Artificial
FRATURE:
CTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 119, Application US/10188832; Publication No. US20040076955A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 AGAARASGPGGGAPR 62
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; ORGANISM: Homo sapiens
US-10-188-832-139
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US-10-777-053-11
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                                                                                                                                               US-10-657-022-74

i Sequence 74, Application US/10657022

is Publication No. US20040180354A1

i GENERAL INFORMATION:

i APPLICANT: Simmard, John J. L.

i APPLICANT: Liu, Liping

APPLICANT: Liu, Zheng

i TILE REFERENCE: MANNK.032A

CURRENT APPLICATION: EPITOPE SEQUENCES

FILE REFERENCE: MANNK.032A

CURRENT APPLICATION NUMBER: US/10/657,022

CURRENT PILING DATE: 2003-09-04

i PRIOR FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610

SEQ ID NO 74

LENGTH: 180

LENGTH: 180
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Best Local Similarity 100.
Matches 15; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM
COMPUTER: Word
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFTCATION BATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: SEPTEMBER: 09/05,423
FILING DATE: SCOTCHOPT IS 1997
APPLICATION NUMBER: 08/937,263
FILING DATE: COCCOBER: 1,1997
APPLICATION NUMBER: 08/925,182
FILING DATE: OCCCOBER: 3, 1996
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SEQ ID NO 11
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, Norman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-10-751-088-15
Sequence 15, Application US/10751088
Publication No. US20040188044A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 180 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 15
                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-10-777-053-11
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48 AGAARASGPGGGAPR
 TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-11-021-441-28
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 SEQ ID NO 7
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Sequence 496, App
Sequence 20556, A
Sequence 22333, A
Sequence 22332, A
Sequence 22661, A
Sequence 22661, A
Sequence 22661, A
Sequence 23906, A
Sequence 5, Appli
Sequence 17631, A
Sequence 25787, A
Sequence 17631, A
Sequence 25787, A
Sequence 17631, A
Sequence 25787, A
Sequence 25787, A
Sequence 25787, A
Sequence 25787, A
Sequence 17631, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 46, Appli
Sequence 47, Appli
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                                                                                             March 13, 2006, 19:54:06; Search time 10.2353 Seconds (without alignments) 40.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                               161667 segs, 27834885 residues
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                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                    1 AGAARASGPGGGAPR 15
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                        Sequence:
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No.
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Sequence 24201, A Sequence 8816, Ap Sequence 14203, A Sequence 19104, A Sequence 1918, App Sequence 19986, A Sequence 19985,
                                          38, Appl
38, Appl
55, Appl
1240, Ap
108, Ap
107, Ap
167, Ap
14205, A
14205, A
14201, A
14201, A
                                          Sequence
Sequence
Sequence
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Sequence 1
Sequence 1
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Sequence
Sequence
                Sequence
US-11-087-099-6009
US-11-096-568A-27265
US-11-096-568A-27265
US-10-921-793-38
US-10-921-793-38
US-11-186-284-65
US-11-186-284-65
US-11-129-143-108
US-11-129-143-108
US-11-129-143-108
US-11-1096-568A-22026
US-11-096-568A-14205
US-11-096-568A-14203
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19104
US-11-096-568A-19108
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Sequence 28, Application US/11021441
| Publication No. US20050249748A1
| Publication No. US20050249748A1
| GENERAL INFORMATION
| APPLICANT: DUBENSKY, Thomas W., Jr.
| APPLICANT: DUBENSKY, Thomas W., Jr.
| APPLICANT: COCK, David N.
| APPLICANT: COCK, David N.
| TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: 282172003900
| CURRENT APPLICATION NUMBER: US/11/021,441
| CURRENT PLING DATE: 2004-12-23
| PRIOR FILING DATE: 2004-10-06
Sequence 7, Application US/11155288
Publication No. US2006008468A1
GENERAL INFORMATION
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANAINT. SIMBLE
TITLE OF INVENTION: ANAINT. SOBA
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR PILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             °,
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US-11-096-568A-22334

Sequence 22334, Application US/11096568A

Sequence 22334, Application No. US2060048240A1

Sequence 22334, Application No. US20600048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22334

LENGTH: 353
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Sequence 22333. Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITIE OF INVENTION: Therby
TITIE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22333
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                                                                                                                                                                                                                          Score 53; DB 7;
Pred. No. 3.3;
0; Mismatches
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Pred. No. 3.8;
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i LOCATION: (1)..(358)
cother information: Ceres Seq. ID no. 12408543
US-11-096-568A-22333
                                                                                                    NAME/KEY: misc_feature
i LOCATION: (1)..(306)
i OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-5688-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
i LOCATION: (1)...(1533)
cother information: Ceres Seq. ID no. 12408544
US-11-096-5688-22334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays subsp. mays
                              TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.9%;
Best Local Similarity 71.4%;
Matches 10; Conservative (
                                                                                                                                                                                                                            67.9%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GAARGOGPGGEOPR 120
                                                                                                                                                                                                                                                                                                                                                          | ||| ||| |||
89 GVARADGPGTGAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAARASGPGGGAPR 15
                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.9
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                              2 GAARASGPGGGAP 14
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Best Local Similarity
       LENGTH: 306
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SEQUENCE CONTRIBUTION: Sequence Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Theory

FILE REPERENCE: 2750-1522032

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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Sequence 496, Application US/10623155

Publication No. US20850261166A1

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong

APPLICANT: Retter, Marc W.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C20

CURRENT APPLICATION NUMBER: US/10/623,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 78; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.0017; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

84.6%; Score 66; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 13; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-08-05
PRIOR PILING DATE: 2004-08-05
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-33
PRIOR PILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
SOFTWARE: PRIOR FILING DATE: 2004-06-30
SOFTWARE: 2004-03-26
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AGAARASGPGGGAPR 122
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGAARASGPGGGAPR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 275-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22661
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JANANA INCOMPANIENT A PRESENTATION, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10542
LENGTH: 167
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 391;
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60.9%; Score 47.5; DB 7;
Best Local Similarity 73.3%; Pred. No. 9.9;
Matches 11; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 48; DB 7;
68.8%; Pred. No. 18;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                         , LOCATION: (1). 7(391)
; OTHER INFORMATION: Ceres Seq. ID no. 12409618
US-11-096-568A-22661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
; LOCATION: (1).:(167)
; OTHER INFORMATION: Ceres Seq. ID no. 13596390
US-11-096-5688-10542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3295, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGAARASGPG--GGAP 14
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66 AGAARRAGPSAPGGAP 81
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.5
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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                                                                                                                                                                                          Sequence 22332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION WUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22662
LENGTH: 359
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       Gaps
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
61.5%; Score 48; DB 7;
Best Local Similarity 68.8%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)..(420)
; JOHER INDORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)._(359)
OTHER INFORMATION: Ceres Seq. ID no. 12409619
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22662, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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; Sequence 22661, Application US/11096568A
; Publication No. US20060048240A1
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ORGANISM: Zea mays subsp. mays
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34 AGAARRAGPSAPGGAP 49
                                                                                      112 GAARGOGPGGEOPR 125
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174 GAARGQGPGGEQPR 187
                                             2 GAARASGPGGGAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAARASGPGGGAPR 15
  Conservative
                                                                                                                                                                                 US-11-096-568A-22332
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 22332
  10;
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Matches
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1 AGAARASGPGGGA 13
                           47 AGAAQPEGPGGAA 59
                                                                                                           RESULT 13
US-11-096-568A-23806
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APPLICANT: Ozenberger, Bradley A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Malkewski, Eileen M.
APPLICANT: Malker, Stephen G.
APPLICANT: Malker, Stephen G.
APPLICANT: Howland, David
APPLICANT: Munber: US 100 (AMP98126P2 C1)
CURRENT APPLICATION NUMBER: US 09/174,936
PRIOR APPLICATION NUMBER: US 09/774,936
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 1998-10-14
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 60/064,583
PRIOR PRILOR DATE: 1998-04-15
PRIOR PRILOR DATE: 1998-04-15
SEQUIN SEQ ID NOS: 52
SOPTWARE: PatentIn version 3.2
SEQUIN DNOS: 52
SEQUIN DNOS: 52
LENGITH: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                            APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: 064335-0191
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALCHIN VET. 2.1
SEQ ID NO 3295
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.3%; Score 47; DB Best Local Similarity 69.2%; Pred. No. 14; Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577 AGAARPEGAAKPPRPRAAGPGGGWP 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10892379
Publication No. US20050282999A9
GENERAL INFORMATION:
                    IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-11-072-512-3295
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US-10-892-379-5
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  APPLICANT
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Sequence 23806, Application US/11096568A
| Publication No. US20060048240A1
| Sequence 23806, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF ERQ ID NOS: 34471
| SEQ ID NO 23806
| LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-05-568A-25788
Sequence 25788, Application US/11096568A
Sequence 25788, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: US/11/096,568A
TITLE OF INVENTION NUMBER: US/11/096,568A
TOTRENT APPLICATION NUMBER: US/11/096,568A
TOTRENT PILING DATE: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 287
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Pred. No. 13;
1; Mismatches
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; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
i_LOCATION: (1).7(287)
cother indexation: Ceres Seq. ID no. 13493532
US-11-096-568A-25788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 7
Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
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72.7%;
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75.0%;
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Best Local Similarity 75.0.
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69 ARGAGPGAGAP 79
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby
PILE REFERENCE: 275-0-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 17631
LENGTH: 293
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JOCATION: (1)...(293)

OTHER INFORMATION: Ceres Seq. ID no. 12359516

FEATURE:

NAME/KEY: misc_feature

JOCATION: (6)...(6)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (70)...(77)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (78)...(78)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (79)...(78)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (81)...(79)

OTHER INFORMATION: Xaa is any aa, unknown or other

FEATURE:

NAME/KEY: misc_feature

JOCATION: (81)...(81)

OTHER INFORMATION: Xaa is any aa, unknown or other

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JOCATION: (81)...(81)
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ORGANISM: Zea mays subsp. mays
FEATURE:
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March 13, 2006, 18:52:59 ; Search time 105.412 Seconds (without alignments) 58.355 Million cell updates/sec
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	OI	AAY05986	AAY05978	AAY05979	AAU85105	ADK68648	AAW62584	AAW69665	AAY05965	AAY52430	AAY70862	AAB03154	AAB69946	AAG67164	AAU01535	AAE07714	AAU84818	AAU11543	ABR58672	ABR48210	ABU56508	ABU56694	ABP74198	ABU64816
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LT 1 15986 AAY05986 standard; peptide; 14 AA. AAY05986;	16-AUG-1999 (first entry)	Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.	NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; hu leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung ca metastessie; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian canc cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; sarcoma; tumour; diagnosis; immunotherapy; the
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ALIGNMENTS

cer; cancer; erapy; uman; ancer; vaccine.

Homo sapiens.

(USSH ) US DEPT HEALTH & HUMAN SERVICES. 97US-0061428P. 98WO-US019609. Wang RF, Rosenberg SA; WPI; 1999-277270/23. WO9918206-A2 21-SEP-1998; 08-OCT-1997; 15-APR-1999. 

The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human BSO-1/CAG-3 (or CAG-3) ORP1 (see AAV05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORP1, CAG-3 ORP2 (see AAV05966), portions of them and their variants (see AAV05967-8F), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of

Abr83438 Human NY-

180 6 ABR83438

74 100.0

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Claim 25; Page 50; 88pp; English. Cancer antigen NY ESO1/CAG-3.

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the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HiA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; Tung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prosestate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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Pred. No. 0.0051;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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                                                                                                                                                                                      return to a patient
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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), and and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precencer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide. The cancer beptide or tumour antibadies reacting with a CAG-3 cancer peptide.

Cor tumour antibadies reacting with a CAG-3 cancer peptide. Useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an LAG annear such as primary or metastatic melanoma, thymoma, lymphoma, cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
                                                                                                                                                                                                                 ö
                  lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, ecritcal cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
derived from, cancers such as primary or metastatic melanoma, thymoma
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidhey cancer; pancreatic cancer; liver cancer; garcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                                          Score 74; DB 2; Length 15;
Pred. No. 0.0055;
Hismatches 0; Indels
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Best Local Similarity luv...
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                                                                                                                                                                                                                                                        1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-277270/23
                                                                                              return to a patient
                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY05979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine.
                                                                                                                                                                                                                                                                                                                                                         RESULT 3
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several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polymuclecitide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptide and polymuclecities are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for are referred to as a Savine. The synthetic polypeptide is useful for cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, concestions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human computations virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory synctytal virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, columnoclia, Streptococcal, Legionella and Mycobacterium or parasitic
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prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection;
                                                                                                                                                                       ö
                                                                                                                         100.0%; Score 74; DB 2; Length 20; 100.0%; Pred. No. 0.0071; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 27; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma; Toxoplasma; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2001; 2001WO-AU000622.
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                                                                                                                                                                                                         1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                   7 GAARASGPGGGAPR 20
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                                                                                                                         Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NYNSOla segment 4.
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N-PSDB; ABK36925.
                                                                                    Sequence 20 AA;
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                                           patient
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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome; under conditions that support processing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasoracide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine development or in the generation or expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunotherapy. The invention is also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitope liberation, substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
(e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence a peptide derived from a parent protein used to construct a savine of
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                                                                                                                               5; Length 30;
                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Epitope liberation-related NY-ESO-1 protein SeqID11.
                                                                                                                           100.0%; Score 74; DB 5; 100.0%; Pred. No. 0.01; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                             ADK68648 standard; protein; 179 AA.
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                                                                                                                                                                                                                                     GAARASGPGGGAPR 19
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                            Similarity 100.
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N-PSDB; ADK68674.
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DIAMOND D C
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                                                                                           Sequence 30 AA;
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                                                        invention
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Best Local S
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(DIAM/)
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                                                                                                                                                               Matches
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for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing target cells in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated cancer associated antigen - is used to develop products for diagnosis and treatment of cancers and for monitoring cancer therapy
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          antigen; NY-ESO-1; regression; progression; onset;
                                                                                                                                                                                       ;
                                                                                                                                                     100.0%; Score 74; DB 8; Length 179; llarity 100.0%; Pred. No. 0.052; Conservative 0; Mismatches 0: ThAPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "potential myristorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                              AAW62584 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                Cancer associated antigen NY-ESO-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US016335.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; treatment; diagnosis
                                                                                                                                                                                                                 1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1998-286417/25.
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                                                                                                                                                                       Best Local Similarity
Matches 14; Conserv
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                                                                                                                                Sequence 179 AA;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer
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                                                                                                                                                                                                                                                                                    RESULT 6
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describes LAGE-1 tumour associated protein (TAP). The present invention which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes LAGE-1 tumour associated protein (TAP). The present invention characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells care specific for complexes of an HLA molecule and a LAGE-1 TAP or an characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an especific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells can be used for the isolated population of T cells with the cytolytic T cells.
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of onset of a cancerous condition, comprising monitoring a sample from a parameter selected from NY-BSO partient with the cancerous condition for a parameter selected from NY-BSO 1 protein, a peptide derived from NY-BSO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-BSO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents human NY-ESO-1, formerly known as LL-1.2
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products for the diagnosis and treatment of LAGE-1 associated disorders,
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
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                                                                                                                                                                                                                                 100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 57-58; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW69665 standard; protein; 180
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                                                                                                                                                                                                                                                                              Conservative
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N-PSDB; AAV50348.
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                                                                                                                                                                                                                                                    Local Similarity
ses 14; Conserv
                                                                                                                                                   therapeutic regime
                                                                                                                                                                                            Sequence 180 AA;
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Matches
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Query Match
Best Local Similarity
Matches 14; Conserv
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15-FEB-2000
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Unidentified
                                                                                                                                                                                                                         AAY52430;
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Peptide
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                                                                                                                                                                                                          The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content ratigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides comprising ORF1, ORF2 (see CAY05966), portions of these peptides and their variants (see AAY05965).

AAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of the cancer peptide, and methods of the cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, concurred from, cancers such as primary or metastatic melanoma, thymoma, corruption and cancer, bladder cancer, leve cancer, leve cancer, leve cancer, leve cancer, leve as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is concurred to the cancer of th
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                                                                                                                                                                                                                                                                                                                                                                            NY ESO-1/CAG-3 gene, CAG-3 gene, cancer antigen, human, leukaemia, non-Hodgkins lymphoma, Hodgkins lymphoma, lung cancer, metastasis, malanoma, adenocarcinoma, thymoma, colon cancer, uterine cancer, breast cancer, prostate cancer, covarian cancer; cervical cancer, bladder cancer, kidney cancer, pancreatic cancer, liver cancer; tumour, diagnosis, immunotherapy, therapy, vaccine, ORFI.
                                                                                                             Gaps
diagnosis and treatment of LAGE-1 associated disorders, particularly
                                                                                                             ö
                                                                            100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                   AAY05965 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US019609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0061428P
                                                                                                                                         1 GAARASGPGGGAPR 14
                                                                                                                                                                      49 GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  return to a patient
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX58599
                                               Sequence 180 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9918206-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                   16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1997;
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                                                                                                                                                                                                                                                                                    AAY05965;
                                                                         Query Match
Best Local &
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                 tumours
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                                                                                                          Matches
                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                          Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .118
== "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Peptide presented by MHC Class I HLA-A24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Peptide presented by MHC Class I HLA-B7"
/note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Peptide presented by MHC Class I HLA-B7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Peptide presented by MHC Class I HLA-A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Peptide presented by MHC Class I HLA-B7"
                                                        ;
                  Length 180;
100.0%; Score 74; DB 2; Length 180 100.0%; Pred. No. 0.052; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   presented by MHC Class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .69
.e= "Peptide presented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .68
e= "Peptide presented by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                 AAY52430 standard; protein; 180 AA.
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--- "Peptide r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .96
... "Peptide F
                                                                                                                                                                                                                                                                                                                                                                        Human tumour antigen NY-ESO-1.
                                                                                               14
                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                      14; Conservative
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82 .90
                                                                                             1 GAARASGPGGAPR
                                                                                                                                  GAARASGPGGGAPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 92
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Gaps

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100.0%; Score 74; DB 3; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indel8

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concoding which was isolated from an oesophagus squamous cell cancer only allowary. Tissue localisation studies revealed it to be expressed at high levels in normal overly and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY ESO-1 are bound by both MHC (major histocompatibility complex) Class I wolecules for presentation to T-cells. Peptides AAY5431-Y5434 bind to Class I HLA-2 molecules, thereby stimulating proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepstoma, ovarian cancer, thyroid cancer, pladder cancer, or lymphoma) and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1998;
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Klade C;

99WO-EP007832, 98EP-00119583

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NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schrier PI, Aarnoudse CA, Heider K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 62-63; 73pp; English.
                                                                                                                                                           AAY70862 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYHO-) UNIV HOSPITAL LEIDEN
                                                                                    49 GAARASGPGGGAPR 62
                                                          1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                   31-JUL-2000 (first entry)
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-339685/29.
N-PSDB; AAD00152.
                                                                                                                                                                                                                                                                                                                                                                WO200023584-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                            27-APR-2000.
                                                                                                                                                                                      AAY70862;
                                                                                                                                RESULT 10
                                                                                                                                               AAY70862
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                                                                                    요
                                                                                                                                   /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
B52"
                                                                                                                                                                                                                                                                           'note= "Peptide (AAY52434) presented by MHC Class I HLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      old LJ;
                            note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                              "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                162. .170
/note= "Peptide presented by MHC Class I HLA-B52"
 "Peptide presented by MHC Class I HLA-B35
                                                                                                                                                                                      "Peptide presented by MHC Class I HLA-B52
                                                                                                                                                                                                                  "Peptide presented by MHC Class I HLA-B52"
                                                                                   /note= "Peptide presented by MHC Class I HLA-B8"
139. .147
                                                                                                                                                                                                                                                                                                              /note= "Peptide presented by MHC Class I HLA-A3"
159. .167
                                                                                                              'note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                  note= "Peptide presented by MHC Class I HLA-A3"
                                                         "Peptide presented by MHC Class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00062422.
98US-00165546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US006875
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                                           .133
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                                                       /note= 138..1
/note=
124. .1
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154. .1
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154. .1
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Gure A, Ritter G;
                                                                                                                                                                          153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038483/03.
N-PSDB; AAZ38380.
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ö The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading from (ORF)-1 that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-asociated antigen and displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or Gaps ö 100.0%; Score 74; DB 3; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels 1 GAARASGPGGGAPR 14 GAARASGPGGGAPR 62 Local Similarity 100. nes 14; Conservative Sequence 180 AA; fusion proteins 49 Query Match ð a

Revised record issued on 21-OCT-2004 : Correction to feature table key

Sequence 180 AA

RESULT 11

Gaps

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Length 180;

100.0%; Score 74; DB 3; Length 18 100.0%; Pred. No. 0.052; .....marches 0; Indels

1 GAARASGPGGGAPR 14

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14; Conservative

Matches

Query Match Best Local Similarity

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New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions.
                                                                                           Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                             /note= "Potential O-phosphorylation site"
152. .172
                                                                                                                                                                                                                         note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                             'note= "Potential O-phosphorylation site"
                                                                                                                                                                             /note= "Potential N-myristoylation site"
                                                                                                                                                                                                  note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                            /note= "Potential transmembrane domain"
                                                                        Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                   'note= "Potential O-phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Y, Tureci O,
                                                                                                                                                                                                                                                                                                                                                                                                             (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOIND INC
                                                                                                                                                         'Location/Qualifiers
         AAB03154 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                               96US-00725381.
                                                                                                                                                                                                                                                                                                                                                                          98US-00013150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gure AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-410880/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA61483.
                                                                                                                                                                  Modified-site
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                                                    23-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scanlan M,
                               AAB03154;
AAB03154
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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a cDNA library prepared from a specimen of well-to-moderately differentiated grammance call cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophagaal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, withous, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The antigen is useful as an immunogen when combined with an adjuvant, in both procursor and post- translationally modified forms, and may be used to precursor and post- translationally modified forms, and may be used to marker for oesophageal cancer, and can be utilised as a marker for the translationally and can be utilised as a marker for the translation and can be utilised as a marker for the translation. can also be used to generate diagnostic or therapeutic agents

Sequence 180 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is human NV-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining whether a cancerous condition is progressing, regressing o remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                        Human, NY-BSO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 74; DB 4; Length 180; 100.0%; Pred. No. 0.052; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                           AAB69946 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Old LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00359503.
                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000; 2000WO-US019220.
GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 GAARASGPGGGAPR 62
                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                         Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jager E, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF58634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                            WO200107917-A1
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUL-1999;
                                                                                                                                                          27-APR-2001
                                                                                                                                                                                                                                                                                                                                                            01-FEB-2001.
                                                                                                                           AAB69946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                         AAB69946
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Matches
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HXXXH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLA-DR; cancer; muman leukocyte antigen-determining region; disease progression; disease regression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents cancer testis tumour antigen NY-ESO-1 dates called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                          Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
                                                                                                                                                                                                                                                                                                                             Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                       Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 4; Length 180;
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NY-ESO-1 tumour rejection antigen precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU01535 standard; protein; 180 AA.
                           AAG67164 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                       for diagnosing testicular tumors.
                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                               22-JAN-2001; 2001WO-US002126
                                                                                                                                                                                                                                    22-FEB-2000; 2000US-00510635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                           Boon-Falleur
                                                                                                                                cancer; testis tumour.
                                                                                                                                                                                                                                                                                               2001-550091/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                        N-PSDB; AAH75118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180 AA;
                                                                                                                                                                       WO200162917-A1
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                    13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2001
                                                                                                                                                                                           30-AUG-2001
                                               AAG67164;
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                                                                                                                                                                                                                                                                          Lethe B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXXXXXXXXXXXXXXXX
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The sequence represents a human NY-ESO-1 tumour rejection antigen or precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leuknoter, expressed in molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC class II HLA-DR.NY-ESO-1/SSX-2 complex expressed on the surface of a cell cor present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the concer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the Concer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the Concert and addition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper I cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                              note= "Phosphorylated"
                                                                                                                                                                                                                                                      'note= "Phosphorylated'
                                                                                                                                                                                                                                                                                                                         'note= "Phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                     /note= "Phosphorylated"
                                                               'note= "Myristoylated"
                                                                                                                              'note= "Myristoylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tureci O, Sahin U, Pfreundschuh M;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE07714 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2000; 2000WO-US026411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00408036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-266156/27.
N-PSDB; AAS02254.
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tes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200123560-A2
          Key
Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                             Modified-site
                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2001
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The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes (TC mV NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP crestricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection from metastasis, or by inhibiting the growth of cancer and protection agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NY-ESO cancer peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.
                                                 Human; major histocompatibility complex; MHC; vaccine; metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic;
                                                                                                                                                                                                               Location/Qualifiers
45. .47
/note= "Encoded by CCCGGGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeng G;
                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2000; 2000US-0179004P.
29-SEP-2000; 2000US-0237107P.
                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2001; 2001WO-US002765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-496851/54.
N-PSDB; AAD14179, AAD14180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang R, Rosenberg SA,
              Human NY ESO-1 protein.
                                                                                                                                                                                                                                    Misc-difference 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 AA;
                                                                                                                                                                                                                                                                                              WO200155393-A2
                                                                                                                                  immunotherapy
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAARASGPGGGAPR 14 ||||||||||||| 49 GAARASGPGGGAPR 62

8 8

Search completed: March 13, 2006, 19:03:59

Job time : 105.412 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24 ; Search time 16.6353 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-27 74 1 GAARASGPGGGAPR 14 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result No.	Score	절	Length	DB	ID	Description
-	50	67.6	82	2	T04476	acclimation protei
~	49	66.2		~	T36115	probable oxidoredu
٣	48	4		~	S50754	hypothetical prote
4	48	4		7	T35694	ATP dependent DNA
s	45	60.8		~	AB3648	flagellar basal-bo
9	44.5	60.1	266	~	T21096	hypothetical prote
7	44.5	60.1	692	N	T21095	
œ	44.5	60.1		7	A36226	collagen alpha 1 c
6	44	59.5		~	E72464	hypothetical prote
20	44	59.5		~	A47008	transcription acti
11	44	59.5		~	S04673	H+-transporting tw
12	44	59.5		-	A48082	MAP kinase 3 (EC 2
2	44	59.6	900	~	B70694	
14	44	59.5		7	F87103	initiation factor
27	44	59.5	-	~	A41350	adenylate cyclase
9	44	59.5	3190	~	T13828	CREB-binding prote
12	43	58.1	185	7	T36874	
81	43	58.1	189	7	AE3136	_
61	43	58.1	189	~	G98151	
20	43	58.1	213	7	S42585	o,
21	43	58.1	260	N	T32525	hypothetical prote
22	43	58.1	307	~	B72677	
23	43	58.1	349	~	S55626	
24	43	58.1	377	~	S28184	_
25	43	58.1	380	~	JC1451	Ca2+/calmodulin-de
56	43	58.1	571	~	I37405	polypeptide N-acet
23	43	58.1	627	~	T35608	polyketide hydroxy
88	43	58.1	619	~	S02165	regulatory protein
62	43	58.1	954	7	A87431	regulatory protein

DNA-binding protei	nitrogen regulator	hypothetical glyci	ovo protein - frui	peptidyl-tRNA hydr	conserved hypothet	hypothetical prote	FRAT2 protein - hu	tail fiber protein	hypothetical prote	homeotic protein e	myristylated alani	aldose 1-epimerase	endopeptidase Clp	hypothetical prote	conserved hypothet
A56038	A34755	B70807	S16356	H87399	G75519	G72663	JC7618	TLBP2X	T29031	C48423	S08341	C87425	T52451	T15143	T36104
7	-	N	7	7	N	7	N	Н	~	~	~	~	~	~	0
1028	1036	1079	1213	143	166	201	233	266	327	333	335	378	387	435	436
58.1	58.1	58.1	58.1	8.95	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8	56.8
43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42

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A;Cross-references: UNIPROT:Q40033; UNIPARC:UP1000009CE5A; EMBL:X97917; NID:g1418969; P b. Experimental source: cv. Igri
C;Genetics:
A;Gene: blt14.2
          C;Species: Hordeum vulgare (Darley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Accession: T04476
A;Accession: T04476
A;Accession: Dina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 2
Pred. No. 4.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2'
acclimation protein 2 - barley
                                                                                                                                                                                                                                                                    A; Residues: 1-82 <PHI>
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|||| :| ||| | 31 GAARGAGAGGGVP 43 1 GAARASGPGGGAP 13 ઠ 셤

probable oxidoreductase - Streptomyces coelicolor

C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C; Accession: T36115
R; Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A; Reference number: 221597
A; Reference number: 221597
A; Accession: T36115
A; Accession: T36115
A; Accession: UNIPROT: 09X887; UNIPARC: UPI0000DB008; EMBL: AL049707; PIDN: CAB41281
A; Experimental source: strain A3(2)
C; Genetics: SCOBDB: SCE15.12c
C; Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

ö Gaps ö Query Match 66.2%; Score 49; DB 2; Length 222; Best Local Similarity 69.2%; Pred. No. 14; Mismatches 3; Indels Matches 9; Conservative 1; Mismatches 3; Indels

1 GAARASGPGGGAP 13

Gaps

; 0

Length 173;

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-692 <MIL>
A;Residues: U-692 <MIL>
A;Cross-references: UNIPROT:Q19579; UNIPARC:UPI000079A30; EMBL:Z50110; PIDN:CAA90444.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-566 <WIL>
A;Cross-references: UNIPROT:Q19581; UNIPARC:UP10000079311; EMBL:Z50110; PIDN:CAA90446.1
A;Experimental source: clone F18H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: X
A,Introns: 111/1; 215/2; 469/3; 552/3
C,Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
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62.5%; Pred. No. 1.2e+02;
7ative 0; Mismatches 3;
                                                                                                                                                        60.8%; Score 45; DB 2;
64.3%; Pred. No. 37;
iive 0; Mismatches
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A,Molecule type: DNA
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A;Accession: T21096
                                                                                                               Query Match
Best Local Similarity
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A, Gene: CESP: F18H3.3b
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    C;Genetics:
A;Gene: BMEII1107
A;Map position: II
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                                                                                                                                                                                                                                                                        C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
E;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, P.M.; Goodenough, U.W.; Haring, Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754
A;Reference number: S50754
A;Accession: S50754
A;Molecule type: mRNA
A;Reference number: John A;Reference n
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R; Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submiris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submiris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A; Reference to the EMBL Data Library, July 1998
A; Reference to the EMBL Data Library, July 1998
A; Accession: T35694
A; Accession: T35694
A; Residues: 1-1690 cHAR>
A; Residues: 1-1690 cHAR>
A; Residues: 1-1690 cHAR>
A; Residues: Laferences: UNIPROT: 086821; UNIPARC: UPIONOODBACB6; EMBL: AL031031; PIDN: CAA19862.
C; Genetics:
A; Experimental Source: Strain A3(2)
C; Genetics:
A; Genetics:
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, f. Mazur, M.; Golteman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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A, Status: preliminary
A, Molecule type: DNA
A, Medicule type: DNA
A, Residues: 1-173 «KUR»
A, Residues: 1-173 «KUR»
A, Cross-references: UNIPROT: 08YAZ4; UNIPARC: UPI0000058740; GB: AE008918; PIDN: AAL54349.1;
A, Experimental source: strain 16M
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                           hypothetical protein WP6 - Chlamydomonas eugametos
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1437 GSANGSGPEGSAPR 1450
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Best Local Similarity 69.2%;
Matches 9; Conservative
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181 GSARASGPSAGRP 193
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Best Local Similarity 64.3%;
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A;Molecule type: mRNA
A;Residues: 1-379 <CHA>
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les 9; Conservative
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                                                                                                                                                                                                             A; Molecule type: DNA
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A;Cross-references: UNIPROT:Q26052; UNIPARC:UPI000007B305; GB:M25282; NID:g159957; PIDN:
A;Cross-references: UNIPROT:Q26052; UNIPARC:UPI000007B305; GB:M25282; NID:g159957; PIDN:
A;Note: the authors translated the codon CAG for residue 136 as Leu, and CAF for residue
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology
C;Reywords: coiled coil; extracellular matrix; glycoprotein; triner; triple helix
F;523-730/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiyasi, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                   C;Accession: A36226
R;D'Alession: A36226
R;D'Alessio, M.; Ramirez, F.; Suzuki, H.R.; Solursh, M.; Gambino, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 9303-9307, 1989
A;Title: Structure and developmental expression of a sea urchin fibrillar collagen gene. A;Reference number: A36226; MUID:90083256; PMID:2594770
A;Accession: A36226
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N;Alternate names: d(CCAAT)-enhancer-binding protein delta, (C/EBP delta); transcription
C;Species: Home sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47008; A40225
E;Accession: A47008; A40225
B;Cleutjens, C.B.; van Bekelen, C.C.; van Dekken, H.; Smit, E.M.; Hagemeijer, A.; Wagner
A;Title: The human C/EBP delta (CRP3/CELF) gene: structure and chromosomal localization.
A;Reference number: A47008; MUID:93300531; PMID:8314590
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A;Molecule type: DNA
A;Residues: 1-220 <KAW>
A;Residues: 1-220 <KAW>
A;Cross-references: UNIPROT: Q9Y9C7; UNIPARC: UP1000005E2F9; DDBJ:AP000064; NID: 95105945;
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collagen alpha 1 chain - sea urchin (Paracentrotus lividus)
C;Species: Paracentrotus lividus (common urchin)
C;Date: 04-Oct.1991 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
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C'Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels E
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A,Gene: APE2360
C,Superfamily: Aeropyrum pernix hypothetical protein APE2360
C,Superfamily: Aeropyrum pernix hypothetical protein APE2360
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Pred. No. 62;
2; Mismatches
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ilarity 57.1%;
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GATRVARPGGGSDR 195
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Best Local Similarity 61.1.
Pest Local 11; Conservative
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Matches 8, Conserv
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A;Status: preliminary
A;Molecule type: DNA
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A.Cross-references: UNIPROT: P49716; UNIPARC: UPI00001274A2; GB:S63168; NID:g386449; PIDN A.Experimental Bource: prostate carcinoma cell line LANCap A;Note: sequence extracted from NCBI backbone (NCBIN:134356, NCBIP:134357)
R;Kinoshita, S.; Akira, S.; Kishimoto, T. Proc. Natl. Acad. Sci. U.S.A. 89; 1473-1476, 1995
A;Title: A member of the C'BEP family. NF-IL6 beta, forms a heterodimer and transcripting A;Reference number: A40225; MUID:92159071; PMID:1741402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1,'T',3-12,'G',14-269 <KIN>
A;Cross-references: UNIPARC:UP10000053FFB; GB:M83667; NID:g189175; PIDN:AAA59927.1; PID
A;Note: sequence extracted from NCBI backbone (NCBIN:82662, NCBIP:82663)
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(s) Species: Homo sapiens (man)
(c) Species: Homo sapiens (man)
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(c) Sates: Homo sapiens
(c) Sates: Homo sapiens
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A;Cross-references: UNIPARC:UNIPARC:UP10000126582
A;Cross-references: UNIPAROT:P05436; UNIPARC:UP1000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Superfamily: H(+)-transporting ATP when synthase; membrane-associated complex
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A;Cross-references: GDB:132661; OMIM:116898
A;Map position: 8q11-8q11
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Keywords: leucine zipper; transcription regulation
F;226-254/Region: leucine zipper motif
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Pred. No. 73;
0; Mismatches
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Search completed: March 13, 2006, 19:16:10 Job time : 16.6353 secs
                                                                      59.5%;
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Best Local Similarity 80.0.
2. 8; Conservative
                                                           Query Match
Best Local Similarity 71.4'
Matches 10; Conservative
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nes 10; Conser
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A;Status: preliminary
A;Molecule type: DNA
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Dates: Mycobacterium tuberculosis
C;Dates: Mycobacterium tuberculosis
C;Dates: Mycobacterium tuberculosis
C;Dates: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajunteam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Atticle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Accession: B70694
A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Residues: 1-900 <COL>
A;Genetics:

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Genetics:

Genetics:

A,Gene GBS:PRKM3; ERKI

A,Cross-references: GBB:135679; OMIM:601795

A,Map position: 16pter-16qter

CyComplex: monomer

C;Function:
A,Pathway: MAP Kinase cascade

C;Superfamily: kinase ralated transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; phosphotransferase; serine/threonin-
A;Pathway: MAP kinase ralated transforming protein; protein kinase homology
C;Superfamily: kinase ATP-binding motif
F;40-330/Domain: protein kinase homology <KIN>
F;40-530/Domain: protein kinase ATP-binding motif
F;202/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted
F;204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase)
A;Cross-references: UNIPROT:P27361, UNIPARC:UP10000035BE2; EMBL:X60188; NID:g31220; PIDN A;Experimental source: hepatoma cell line HEP G2 authors translated the codon AGC for residue 17 as Ile F;Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D. Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992 A;Pitle: Extracellular signal-regulated kinases in T cells: characterization of human ER A;Pitle: Extracellular signal-regulated kinases in T cells: characterization of human ER A;Pitle: Extracellular signal-regulated kinases in T cells: characterization of human ER A;Pocession: PQ0270 MUD:92171961; PMID:1540184 A;Pesidues: 14-113,'I', 175-379 <OWA> A;Pesidues: 15-113,'I', 175-370 <OWA> A;Pesidues: 15-113,'I', 175-370 <OWA> A;Pesidues: 15-1
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 25-173,'1',175-379 <GON>
A;Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:923882; PIDN:CAA77754.1; PIII
C;Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).
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F;509-512/Region: GFP-binding NKXD motif
F;545-547/Region: GFP-binding SAK/L motif
F;411,412,432,509,510,512,545/Binding site: Mg-GFP (Ly8, Thr, Thr, Asn, Ly8, Asp, Ser)
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69.2%; Pred. No. 96;
ive 0; Mismatches 4; Indels
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Best Local Similarity 69.20,
Best Local Similarity 69.20,
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initiation factor IF-2 [imported] - Mycobacterium leprae
[5/Species: Mycobacterium leprae
[5/Sude: S.T.; Esglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R;Cole, S.T.; Esglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
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R,Krupinski, J.; Coussen, F.; Bakalyar, H.A.; Tang, W.J.; Feinstein, P.G.; Orth, K.; Sla
Science 244, 1558-1564, 1989
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A,Reference number: A41350; MUID:89298382; PMID:2472670
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A;Molecule type: mRNA
A;Residues: 1-1134 <KKU>A;Residues: 1-1134 <KKU>A;Cross-references: UNIPROT:P19754; UNIPARC:UPI000112886C; GB:M25579; NID:g162612; PIDN
A;Cross-references: UNIPROT:P19754; UNIPARC:UPI00012886C; GB:M25579; NID:g162612; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reaiduea: 1-924 <STO>
A;Cross-references: UNIPROT:Q9Z519; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g13093370;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
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Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                                    4; Indels
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MUCLEOTIDE SEQUENCE.
MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
M. Lesticular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
                                                                                                                                                                                                                                                                                   01-07-2000 (TrEMBLrel. 15, 01-07-2000 (TrEMBLrel. 15, 01-0CT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                            Hypothetical protein LAGE-2
                                    00000000
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ID Q9NY13 HUMAN PRELIMINARY;
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NCBI_TaxID=9606;
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                                                                               March 13, 2006, 18:53:23 ; Search time 101.624 Seconds (without alignments) 97.196 Million cell updates/sec
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
Hypothetical protein.
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15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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Q4RDF1_TETNG
Q4RDF1_TETNG
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Q6 2 DA7_BURPA
Q81619_QRYSA
Q3 9492_CHLEU
Q7R1E3_QRYSA
Q5R1E3_QRYSA
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Homo sapiens (Human).
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1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                             Flatzer M.;
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                          NUCLEOTIDE SEQUENCE
                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                          Platzer M
                                                                                                                         Platzer M
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene reveals an
                                              MEDLINE-98289662; PubMed-9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                    WUCLEOTIDE SEQUENCE.
MEDLINE=98430682; PubMed=9759882;
Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
Schwartzentruber D.J., Rosenberg S.A.;
Schwartzentruber D.J., Rosenberg S.A.;
"A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames.";
J. Immunol. 161:3596-3606 (1998).
-1- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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MEDLINE=21566154; Pubmed=11709543; DOI=10.1093/hmg/10.22.2557;
Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 1; Length 180; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galgoczy P., Rosenthal A., Platzer M.; "Human-mouse comparative sequence analysis of the NEMO gealternative promoter within the neighboring G6PD gene."; Gene 271:93-98(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                     Gly-rich.
; B122C5C2C8BE1569 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
                                                                                   "LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                          Potential
                                                                                                                                                                                                                                                                                                                                 EMBL, U87459; AAB49693.1; -; mRNA.
EMBL; AJ003149; CAA05908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA; 17992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7LBY4_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                     HGNC:2491; CTAG1B
                                                                                                                                                                                                                                                                                                                                                                                     Antigen; Transmembrane.
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                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                     rissum=Melanoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Matches
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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"Multiple pathogenic and benign genomic rearxangements occur at kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 74; DB 2; Length 180; 100.0%; Pred. No. 0.031;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF277315; AAL27014.1; -; Genomic_DNA.
EMBL, A275977; CAB76943.1; -; Genomic_DNA.
EMBL, AF277315; AAL27013.1; -; Genomic_DNA.
SEQUENCE 180 AA; 17992 MW; B122C5CZC8BE1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                          Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
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MEDLINE=98289662; PubMed=9626360;
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                              Trissue=placenta;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Guarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnercth A., Schein J.E., Jones S.J.M., Marra M.A.;

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
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LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=LAGE-1B; Synonyms=LAGE-1L;
ISOId=075638-1; Sequence=Displayed;
Name=LAGE-1A; Synonyms=LAGE-1S.
Name=LAGE-1A; Synonyms=LAGE-1S.
ISOId=075638-2; Sequence=VSP 004301;
ISOId=075638-2; Sequence=VSP 004301;
Some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
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                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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/FTId=VAR_007855.
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/FTId=VAR 007857
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EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
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188
210
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Burkholderiaceae; Burkholderia; pseudomallei group.
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=holA; OrderedLocusNames=BMA2451;
Burkholderia mallei (Pseudomonas mallei)
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative DNA polymerase III.
                                                                                                                                                                                                                                                                                                                                                  25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28,
14
                                                                        49 GAARASGPRGGAPR 62
                                                                                                                                                                                                                                                                 Q63QT8_BURPS PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q62H22 BURMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 ARAAGPGGDAPR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=28450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K96243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BURMA
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Gaps

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Score 66; DB 1; Length 210; Pred. No. 0.42; 0; Mismatches 1; Indels

89.2**%**; 92.9**%**;

Query Match Best Local Similarity 92.9 Matches 13; Conservative

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SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
Hum. Mo 1. Genet. 10:339-352(2001).
EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
Ensembl; RSSG0000167933; Homo sapiens.
SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Zarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Froc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).

FIGR: BMA2451;
FIGR: BMA2451;
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                                                                                                                                                                                                                    GO, GO:0003887, F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR0505790; DNA pol1II delta.
Pfam; PF06144; DNA pol3 delta; I.
IIGREMMs; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              73.0%; Score 54; DB 2; Length 362; 83.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 2; Length 321;
Pred. No. 46;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                            Complete proteome, Nucleotidyltransferase, Transferase. SEQUENCE 362 AA, 38726 MW, D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q$6$27_HUMAN PRELIMINARY; PRT; 321 AA.
Q$6$27;
Q$1_DEC-2001 (TrEMBLrel. 19, Created)
01_DEC-2001 (TrEMBLrel. 19, Last sequence update)
01_MAR_2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.3%;
76.9%;
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09GRA8;

01-MAR-2001 (TrEMBLrel. 16,

01-MAR-2004 (TrEMBLrel. 16,

01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 ARAAGPGGDAPR 359
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Best Local Similarity 76.9
Matches 10, Conservative
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5 AARRAGPGGGAAR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=gene X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q96S27_HU
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Q9GRA8 GR
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Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chow T.-Y., Heing Y.-I.C., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-T., Chang S.-J., Cheng C.-H., Heiso S.-Y., Heiso C.-H., Hang C.-H., Hang S.-Y., Heiso S.-H., Heing J.-N., Heu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F.;

"Oryza sativa BAC OSJNBboll2G21 genomic sequence.";

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AC135421; AAU10755.1; -; Genomic_DNA.
Hedgehog protein (Fragment).
Gryllus bimaculatus (Two-spotted cricket).
Eukaryota, Metazoa, Arthropoda; Haxapoda; Insecta, Pterygota;
Neoptera, Orthopteroidea; Orthoptera, Ensifera, Gryllidae, Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                             MEDLINE=20461145; PubMed=11003837; Misumi Y., Ohuchi H., Niwa N., Inoue Y., Nozawa A., Salto M., Misumi Y., Ohuchi H., Yoshioka H., Noji S.; "Correlation of diversity of leg morphology in Gryllus bimaculatus (cricket) with divergence in dpp expression pattern during leg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GG; GO:000233; F:peptidase activity; IEA.
R GG; GO:0007267; P:cell-cell signaling; IEA.
R GG; GO:0007275; P:cell-cell signaling; IEA.
GG; GO:00016539; P:intein-mediated protein splicing; IEA.
R GG; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR003586; Hedgehog_hint_C.
R InterPro; IPR003209; HH signal.
R InterPro; IPR0001320; HH signal.
R InterPro; IPR001657; Peptidase C46.
InterPro; IPR001657; Peptidase C46.
InterPro; IPR001767; Pept_C46_hint.
R Pfam; PF01089; HH signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 AA; 48008 MW; 29AEFB061C3EE6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 2
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein OSJNBb0012G21.2
Name=OSJNBb0012G21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Development 127:4373-4381(2000).
EMBL; AB044709; BAB19658.1; -; mRNA.
HSSP, 062226; 1VHH.
SMR; O9GRA8; 49-205.
MEROPS; C46.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last seq
25-0CT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00612; SONICHHOG.
MARAT; SN001305; Hainc; 1.
SMART; SN001305; Hintc; 1.
PROSITE; PS50817; INTEIN N_TER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.3%; Scor.
78.6%; Pred
0; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 GAARACGPGRGAGR 43
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Q688JS ORYSA PRELIMINARY;
Q688JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                            development.";
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EMBL; AL354776; CAC17565.2; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buell R.;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
Q6AV33_ORYSA
                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                ö
                                                                                                                                                                                            DB 2; Length 644;
            GO; GO:0004057; F:arginyltransferase activity, IEA.
GO; GO:0016598; P:protein arginylation; IEA.
GO; GO:001276; P:regulation of protein catabolism; IEA.
InterPro; IPR007472; ATE C.
InterPro; IPR007471; ATE N.
Pfam; PF04377; ATE C.
Hypothetical proteIn:
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                          644 AA; 72444 MW; DDB97FC0C40C23F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Contains 2 ANK repeats.
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-PAY-2005 (Rel. 47, Last annotation update)
Name=C20orf86;
                                                                                                                                                                                                                                                                                                                                                                                     337 AA
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                           Pred. No. 88;
                                                                                                                                                                                            Score 52;
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                          70.3%;
                                                                                                                                                                                                           Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                       9 GAASASGPGGG 19
                                                                                                                                                                                                                                                               1 GAARASGPGGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Gramene; Q688J5; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                     CT086 HUMAN
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Q9BZ19;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein OSJNBa0063118.9.
Name=OSJNBa0063118.9.
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantaes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.M., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mitce O., Salzberg S.L., Fraser C.M., G.M., Salzberg S.L., Fraser C.M., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 1; Length 337;
Pred. No. 66;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 2; Length 367;
Pred. No. 71;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                   ANK repeat, Hypothetical protein; Polymorphism; Repeat DOMAIN 88 164 Ubiquitin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         R -> C (in dbSNP:584855).
/FTId=VAR 014400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EC8BA4AD414756CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                Ubiquitin-like.
ANK 1.
ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 AA.
HSSP; P42771; 2ASE.
Ensembl; ENSG000012427; Homo sapiens.
HGNC, HGNC:16217; C20orf86.
InterPro; IPR000526; Ubiquitin.
Pfam; PF00023; Ank; 2.
PRINTS; PR01415; ANK?IN.
SMART; SM00248; ANK; 2.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50299; UBIQUITIN 1; PRLSE_NEG.
PROSITE; PS0089; ANK_REPEAT; 2.
PROSITE; PS0089; ANK_REPEAT; 2.
PROSITE; PS00299; UBIQUITIN 1; PRLSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 AA; 36714 MW;
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76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4%,
Rest Local Similarity 71.4%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||:|| ||| ||
9 GGARAAGPTGGASR 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEAV33 ORYSA PRELIMINARY;
QEAV33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AARASGPGGGAPR 14
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RESULT 12

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Query Match
Best Local Similarity 69.4.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                             Q40033_HORVU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAARASGPGGGAP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GAARGAGAGGGVP 43
                                                                                                                                                                                                                                 9; Conservative
                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       BLT14.2 protein.
Name=blt14.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
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01-JUN-2003
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                                                                                                                                                                                SEQUENCE
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Doverton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                 Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                           The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                      J., Yuan Q.;
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.9%; Score 51; DB 2; Length 559; 64.3%; Pred. No. 1e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA; 58950 MW; A5B4492C2D3F94FA CRC64;
                                                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update) Hypothetical protein OSJNBa0011L09.12.
ORFNames=OSJNBa0011L09.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OSJNBa0026A15.11.
                                                                                                                                                                                                                                                                                                                                                                                                                   Buell C.R., Wing R.A., McCombie W.R., Messing
Submitted (MAY-2003) to the EMBL/GenBank/DBJ
BEBL; AC092388; AMM2719.1; -; Genomic_DNA.
EMBL; AE017090; AAP53592.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867 AA
                  559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                         01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007228; DUF390.
InterPro; IPR007321; Transposase_28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF04094; DUF390; 2.
Pfam; PF04195; Transposase_28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 64.3%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 GGSŘTSCPCGCGSŘ 290
                                                                                                                                                                                                                                                                                                                                                                                Science 300:1566-1569(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ORYSA
Q94LD1 ORYSA PRELIMINARY;
Q94LD1;
00 orysa
Qēl680 orysa preliminary;
Q8l680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                      NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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Matches
                                                                                                                                                                                                                                                                                              Buell
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Q94LD1_ORY
   T RAP RAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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MEDLINE-97299834; PubMed=9154983; DOI=10.1023/A:1005717613224;
MEDLINE-97299834; PubMed=9154983; DOI=10.1023/A:1005717613224;
Phillips J.R., Dunn M.A., Hughes M.A.;
Phillips J.R., Dunn M.A., Hughes M.A.;
Palant Ad. 1810. 33:1013-1023 (1997).
Plant MOL. Biol. 33:1013-1023 (1997).
PRIST, X97917; CAA66490.1; -; Genomic_DNA.
PIR; T04476; T04476.
SEQUENCE 82 AA; 7752 MW; FA952DCA3CD640A7 CRC64;
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Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50, DB 2; Length 82;
Pred. No. 24;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                        Buell R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      1 protein.
867 AA; 92812 MW; 7365009715EDDC21 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Pancreatic duodenal homeobox gene 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 2; I
Pred. No. 1.6e+02;
1; Mismatches 4;
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                                                                                                                                                                                                EMBL; AC084404; AAK50601.1; -; Genomic DNA
                                                                                                                                                                                                                Gramens, Q94LD1; -.
InterPro; IPR007228; DUF390.
InterPro; IPR007321; Transposase_28.
Pfam; PF04094; DUF390; 3.
Pfam; PF04195; Transposase_28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GGSRAGGPGGGGSR 219
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QSNTAS;
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NUCLECTIDE SEQUENCE.
A Takagi K., Neo S., Furuichi M., Watanabe M., Kansaku N., Hisasue M., A Takagi K., Neo S., Furuichi M., Watanabe M., Kansaku N., Hisasue M., A Tsuchiya R., Yamada T.;
Canine Pdx-1."; Canine Pdx-1."; Canine Pdx-1."; Canine Pdx-1."; The EMBL, Gentapases G. Go. 0005634; C. Canine Pdx D. Go. 60.005634; C. Cancleus; IEA.

RW Nuclear protein.
FT NON TER 11 11
FT NON TER 11 111
FT SQ SEQUENCE 111 AA; 11740 MW; 4565A9E8BEDEC91E CRC64;
                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                            Ouery Match 67.6%; Score 50; DB 2; Length 111; Best Local Similarity 64.3%; Pred. No. 32; Matches 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 13, 2006, 19:14:27 Job time : 102.624 secs
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15 GGSRASSPGGAQPR 28
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25611,

Sequence

Sequence 21, Appl Sequence 2410, A Sequence 29442, A Sequence 19030, A Sequence 26, Appl Sequence 27111, A Sequence 27111, A Sequence 27111, A Sequence 25927, A

23, Appl

Sequence

OM protein

Run on:

Sequence:

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100.0%; Score 74; DB 1; Length 180; 100.0%; Pred. No. 0.025; tive 0; Mismatches 0; Indels
US-10-104-047-3295
US-09-902-540-13196
US-09-252-911A-2511
US-09-252-911A-26110
US-09-252-911A-26110
US-09-252-991A-29442
US-09-252-991A-19030
US-08-352-991A-19030
US-08-352-670B-26
US-08-33-5-66-26
US-08-33-5-66-26
US-08-945-128-26
US-09-945-128-26
US-09-945-14030A-26
US-09-252-991A-27111
US-09-252-991A-25227
US-09-252-991A-25227
US-09-252-991A-25927
US-09-252-991A-25927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leth , Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
ATTLE OF INVENTION: Li-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STRRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY, AGENT INPORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08791495
Patent No. Sal1519
GENERAL INFORMATION:
APPLICANT: Leth , Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GAARASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
    MOLECULE TYPE: protein
    USA
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US-08-791-495-9
  US-08-791-495-9
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Sequence 8, Appli
Sequence 15, Appli
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Sequence 9, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 17, Appli
Sequence 17315, A
Sequence 17349, A
Sequence 17249, A
Sequence 17249, A
Sequence 17249, A
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Sequence 30219, A
Sequence 117, App
Sequence 117, App
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Sequence 19752, A
Sequence 32326, A
Sequence 31759, A
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Sequence 31279, 1
Sequence 23998, 1
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                                                                                                                                      March 13, 2006, 19:14:49 ; Search time 26.0235 Seconds (without alignments) 44.477 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2 6/ptodata/1/iaa/5 COMB.pep:*
/cgn2 6/ptodata/1/iaa/6 COMB.pep:*
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US-09-341-829A-9

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US-09-341-829A-7

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US-09-341-829A-7

US-09-252-991A-17249

US-09-252-991A-17249

US-09-252-991A-17249

US-09-252-991A-17249

US-09-252-991A-31279

US-09-344-040C-117

US-09-325-991A-31279

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                                                                                                                                                                                                                                                                                                                                                                        572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
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Minimum DB Maximum DB

Searched:

Database :

Result No.

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Gaps

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amino acid
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COUNTRY:
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                                                                              Sequence 8, Application US/08937263B
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
    APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
    APPLICANT: Alexander; Knuth; Dijfhout, Jan W.
    TITLE OF INVENTION: INSOLATED NUCLEIC ACID MOLECULE
    TITLE OF INVENTION: ITSELF, AND USES THEREOF
    NUMBER OF SEQUENCES: 8
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fulbright & Jaworski, L.L.P.
    STATE: New York
    CONTRY: USA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09751798

Patent No. 6525177

GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth, Jager, Elke;

APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;

APPLICANT: Chuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Antibodies Which End to NY-ESO-1

TITLE OF INVENTION: Associated Proteins, Uses Thereof,

TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA

TITLE OF INVENTION: Binding Peptides Derived Therefrom

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 74; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CODNIKA:
ZIP: 10.10.—
ZIP: 10.10.—
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fith Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: Wordberfect

CURRENT APPLICATION DATA:

PRICE SPECIAL SEPTION TOWNER: US/08/937,263B

FILING DATE: September 15, 1997

PRIOR APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORWATION:

NAME: Sinn, Eric, Patent Agent

REGISTRATION NUMBER: 40,177

REFERENCS/DOCKET NUMBER: 40,177

REFERENCS/DOCKET NUMBER: 1UD 5466.1

TELECOMMUNICATION INFORMATION:

TELEFHONE: (212) 318-3000

TELEFHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAARASGPGGGAPR 14
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                                                                           US-08-937-263B-8
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, All O.
APPLICANT: Gure, All O.
APPLICANT: Gure, All O.
APPLICANT: Gure, All O.
APPLICANT: Glove, All O.
TITLE OF INVENTION: Concer Associated Antigens and Uses;
TITLE OF INVENTION: Therefor;
TITLE OF INVENTION: Therefor;
TITLE OF INVENTION: Therefor;
FILE REPRENCE: L0461/7062;
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT APPLICATION NUMBER: PCT/US98/14679
EARLIER APPLICATION NUMBER: PCT/US98/14679
SOFTWARE: FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
COUNTYER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                               COMPUTER: 150
COMPUTER: 150
COMPUTER: 150
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION NUMBER: 09/062,192
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HARSON, NO. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5466.3
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09392714A Patent No. 6686147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 318-3168
TELEFRAX: (212) 725-5958
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-392-714-25
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Gaps
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    <151> 1998-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-849-602-30
Sequence 30, Application US/09849602
Sequence 30, Application US/09849602
FREAL No. 6794501
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 2; 100.0%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08791495
Patent No. 5811519
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                       14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-341-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02210
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                                                                                                        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811) TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Leth,, Bernard
APPLICANT: Leth,, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE REPREBUCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495 <151> 1997-0
                                                                                                                                                                                                                                                                      ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: OCCODER 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,946
                                      Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 318-3400
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS
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COUNTRY: USA
                       US-09-165-546D-15
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Wolf, Greenfield & Sacks, P.C.

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ADDRESSEE:
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APPLICANT: Leth,, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPERENCE: Lode1/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DS 08/791,495
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                           Query Match

89.2%; Score 66; DB 1; Length 180;
Best Local Similarity 92.9%; Pred. No. 0.25;
Matches 13; Conservative 0; Mismatches 1; Indels
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US-08-791-495-5
Sequence 5, Application US/08791495
Patent No. 5811519
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
APPLIANTE:
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameteradam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 610-10461/7005
TELECOMMUTICATION INFORMATION:
TELEPHONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLLOGY: linear
TOPOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09341829A
Patent No. 6794131
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein
US-08-791-495-7
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-341-829A-7
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; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
   APPLICANT: Lucta, Sophie
; APPLICANT: Lucas, Sophie
; APPLICANT: Godelaine, Daniele
; APPLICANT: Godelaine, Daniele
; APPLICANT: Godelaine, Daniele
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUWOR ASSOCIATED NUCLEIC ACIDS
; FILE REPERENCE: L0461/7066
; CURRENT APLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; NUMBER OF SEQ ID NOS: 14
; NUMBER OF SEQ ID NOS: 14
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Pred. No. 0.28;
0; Mismatches 1; Indels
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          L0461/7005
                                                                    COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ammeterdam, John R.
REGISTRATION NUMBER: 40,212
    600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: LC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO 5; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5
STREET: 600 ..
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Gaps
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                                                                                                                                                                                                                                                                            Score 50; DB 2; Length 160;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-789-329C-10
Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: FOR IMPROVED FOULTRY PRODUCTION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Maingroin, LLP
ADDRESSEE: Maingroin, LLP
ADDRESSEE: Maingroin, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 143;
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                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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COUNTRY: United States of America
ZIP: 9724-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM FC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,329C
FILING DATE: 01/23/97
  FILING DATE: 1998-02-18
APPLICATION NUMBER: US 60/094,190
FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41,401
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01/23/97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BATP, David J.
REGISTRATION NUMBER: 41,40
REFERENCE/DOCKET NUMBER: 2
  PRIOR FILING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17249
LENGTH: 160
TYPE: PRI
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Best Local Similarity 69.2'
E-rhes 9; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-10
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; Sequence 24923, Application US/09252991A
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
    APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC CATC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1999-02-18
; PRIOR PLICATION NUMBER: US 60/094,190
; PRIOR PLICATION DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
     Sequence 17335, Application US/09252991A

Patent No. 6551735

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 1999-02-18

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18
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US-02-252-991A-17249

US-02-252-991A-17249, Application US/09252991A

Padent No. 6551795

GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788
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Pred. No. 16;
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0
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US-09-252-991A-17335
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Best Local Similarity 71.4%;
Matches 10; Conservative
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278 GAGRAAGPGTGQPR 291
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US-09-252-991A-17335
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Search completed: March 13, 2006, 19:18:51 Job time : 27.0235 secs

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Sequence 1404, Application US/10296734

Sequence 1404, Application US/10296734

Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE OF INVENTION: Synthetic molecules and uses therefor CURRENT FILING DATE: 2003-08-04

PRIOR REPERENCE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

LENTH: 30

LENTH: 30
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        US-10-295-027-1388
US-10-188-832-141
US-10-117-937-569
US-10-117-937-75
US-10-117-937-75
US-10-117-937-77
US-10-877-37-77
US-11-067-064-75
US-11-067-064-75
US-11-067-064-75
US-11-067-064-75
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US-11-067-064-75
US-11-067-064-76
US-11-067-159-75
US-11-067-159-75
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US-11-067-159-76
US-11-067-159-76
US-11-067-159-76
US-11-067-169-76
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Sequence 202, Application US/10482029

Fublication No. US20050037445A1

GENERAL INFORMATION:
APPLICANT: ODIN medical A/S

TITLE OF INVENTION: Oncology drug innovation
FILE REFERENCE: P 573 PC00

CURRENT APPLICATION NUMBER: US/10/482,029

CURRENT FILING DATE: 2003-12-29

NUMBER OF SEQ ID NOS: 437

SOFTWARE: Patentin version 3.1

SEQ ID NO 202

LENGTH: 179
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US-10-296-734-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial
 US-10-296-734-1404
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Appli
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Sequence 202, App
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Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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69.096 Million cell updates/sec
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                                                                                    March 13, 2006, 19:51:56; Search time 84.6588 Seconds
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Sequence 3
Sequence 7
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Sequence 2
Sequence 2
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Sequence
Sequence
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!: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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!: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

!: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

!: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

!: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-296-734-1454
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US-09-821-883-27
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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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74
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Perfect score:
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Result No.

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Gaps

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Stockert, Elisabeth
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LENGTH: 180
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US-10-023-182-8
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Sequence 8, Application US/09751798
Sequence 8, Application US/09751798
Sequence 8, Application US/09751798
Setent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth, Jager, Elke;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Associated Porteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: New York City
STATE: New York
COUNTRY: USA
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Query Match 100.0%; Score 74; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 14; Conservative 0; Mismatches 0; Indels
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; Pred. No. 0.14;
0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: OCCODER 3, 1996
ATTORNEY/ACENT INFORMATION:
NAME: Hanson, No. US20020010321Alman
REGISTRATION WIMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERENCE/DOCKET NUMBER: LUD 5466.3 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3168 TELEPHONE: (212) 752-5958 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-02-49-602-30
US-03-499-602-30
; Publication No. US2003016583431
; GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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OPERATING SYSTEM: PC-DOS
                                                                                                                               49 GAARASGPGGGAPR 62
                                                                                                  1 GAARASGPGGGAPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Xnuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodias Which Bind to NY-ESO-1 Cancer;
Truncated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HIA
Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                           ;
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COUNTRY: USA
ZIP: 10103
COMPUTER FADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. US20020164665Alman D. REGIGYRATION UNBER: 30,946
REFERENCE/DOCKET NUMBER: UUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/725,182
FILING DATE: OCTOBER: 1996
ATTORNEY/AGENT INFORMATION:
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
TIER REFERENCE: L0461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPOTECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAARASGPGGGAPR 14
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                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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Gaps
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                      APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: BRITODE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFRENCE: CTLIMM.21CP1C
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT APPLICATION NUMBER: US/061,074
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR APPLICATION NUMBER: 09/561,572
PRIOR PLING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
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Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIU Liping
APPLICANT: SIR, Zhidong
TITLE OF INTWINTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIPM. 027A
CURRENT APPLICATION NUMBER: US/01/11,937
CURRENT FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PLLING DATE: 2001-11-07
PRIOR PLLING DATE: 2001-11-07
PRIOR PLLING DATE: 2002-03-07
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 180
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Matches 14; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 14, Application US/10364614
Publication No. US20030175250A1
Publication No. US20030175250A1
APPLICANT: JAGER, Elke
APPLICANT: GNUTH, Alexander
APPLICANT: GNIJATIC, Sacha
TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
FILE REFERENCE: LO F 72.6.1
CURRENT APPLICATION NUMBER: US/10/364,614
CURRENT PILING DATE: 2003-02-24
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID WOS: 17
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US-10-207-655-71

Sequence 71, Application US/10207655

Sequence 71, Application US/10207655

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.;

APPLICANT: Hadden-Ledbetter, Martha S.;

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS;

FILE REFERENCE: 390069-401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOFTWARE: Patentin version 3.0
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Query Match 100.0%; Score 74; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 14; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.14;
; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
                                                                                                             1 GAARASGPGGGAPR 14
                                                                                                                                                            49 GAARASGPGGGAPR 62
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US-10-207-655-71
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Best Local Similarity
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LENGTH: 180
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LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Marray, Richard
APPLICANT: Marray, Richard
APPLICANT: Marray, Richard
APPLICANT: Wasnen, Susan R.
TITLE OF INVENTION: Methods of Enginesis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: WINDER: US/10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PILING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-11-29
PRIOR PELING DATE: 2001-12-14
PRIOR PELING DATE: 2002-01-10
PRIOR 
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Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOUTHWARE: Patentin version 3.2
                       Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                               APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GAARASGPGGGAPR 62
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ORGANISM: Homo sapiens
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US-10-296-734-832
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yes-10-188-832-139

j Sequence 139, Application US/10188832

j Publication No. US20040076955A1

j GENERAL INFORMATION:

j APPLICANT: Mack, David H.

j APPLICANT: Mack, David H.

j APPLICANT: Bos Biotechnology, Inc.

TITLE OF INVENTION: mad Methods of Diagnosis of Bladder

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: 2002-11-22

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US 60/302,814

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-01-03

j PRIOR FILING DATE: 2001-11-13

SOFTWARE: PAFENTIN NUMBER: US 60/372,246

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PAFENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/1077053

Publication No. US20040132088A1

GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE OF INVENTION: UNMER: US/10/777,053

CURRENT APPLICATION NUMBER: US/10/777,053

CURRENT FILIAG DATE: 2004-02-10

FRICH APPLICATION NUMBER: 10/292,413

PRIOR FILING DATE: 2002-11-07
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                                                                                    ; OTHER INFORMATION: NYNSOla consensus polypeptide US-10-296-734-832
                                                                                                                                                                                                                                                                                                     1 GAARASGPGGGAPR 14
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; ORGANISM: Homo sapiens
US-10-188-832-139
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-188-832-139
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US-10-777-053-11
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                         APPLICANT: Simmard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNK. 032A
CURRENT APPLICATION NUMBER: 05/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 60/409123
PRIOR PLING DATE: 2002-09-06
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: PASESEQ for Windows Version 4.0
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Job time: 85.6588 secs
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; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                               49 GAARASGPGGGAPR
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ORGANISM: Homo sapiens
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Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **
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MEDIUM TYBE: Diskette, 3.5 inch, 144 kb storage computer: IBM OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: APAT1 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: APAT1 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: APAT1 17, 1998
APPLICATION NUMBER: US/997,263
FILING DATE: APAT1 17, 1998
APPLICATION NUMBER: US/997,263
FILING DATE: APAT1 17, 1998
APPLICATION NUMBER: US/997,263
FILING DATE: APATH US/997,263
FILING DATE: APATH US/997,263
FILING DATE: APATH US/997,263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERRENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SSCTWARE: PastSEQ for Windows Version 4.0
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-10-751-088-15
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TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-10-751-088-15
Sequence 15, Application US/10751088
Publication No. US20040158044A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                      1 GAARASGPGGGAPR 14
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                                                                                                                                                  TYPE: PRT; ORGANISM: Homo Sapien
US-10-777-053-11
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TYPE: PRT
ORGANISM: Homo sapiens
LENGTH: 180
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SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 28, Appl
Sequence 496, Appl
Sequence 20556, A
Sequence 22333, A
Sequence 22332, A
Sequence 22332, A
Sequence 2395, Ap
Sequence 3295, Ap
Sequence 34, Appl
Sequence 34, Appl
Sequence 1265, A
Sequence 1265, A
Sequence 1260, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8816, Ap
Sequence 19104, A
Sequence 5, Appli
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Sequence 22661, A
Sequence 26217, A
Sequence 35, Appl
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                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           March 13, 2006, 19:54:06; Search time 9.55294 Seconds (without alignments) 40.793 Million cell updates/sec
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                                                                                                                                                                                                                                                                        Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/USIO NEW PUB.pep:*
       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-021-441-28
US-11-006-568A-20556
US-11-096-568A-22334
US-11-096-568A-22333
US-11-096-568A-22332
US-11-096-568A-22332
US-11-096-568A-23806
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US-11-096-568A-22662
US-11-129-143-108
US-11-096-568A-2662
US-11-129-143-108
US-11-129-143-108
US-11-129-143-108
US-11-1096-566A-22661
US-11-1096-568A-22661
US-11-1096-568A-22661
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US-11-096-568A-19104
US-10-892-379-5
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                    1616b7 segs, 27834885 residues
                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                   1 GAARASGPGGGAPR 14
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Maximum DB seq length: 200000000
                                                                                                   US-09-529-206E-27
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Match Length
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                                                                                                                       Sequence:
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                                                              Run on:
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No.
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145, App
641, App
14, App 1
23045, A
25788, A
12631, A
211931, A
25787, A
21193, A
21193, A
25786, A
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112, App
8, Appli
                                     Sequence Seq
US-11-096-568A-19986
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US-11-096-568A-19984
US-11-096-568A-145
US-11-096-568A-141
US-11-096-568A-1208
US-11-096-568A-2208
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RESULT 2
US-11-021-441-28
US-11-021-441-28
US-11-021-441-28
Sequence 28, Application US/11021441
Publication No. US2055249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DOKTNOY, Daniel A.
TAPLICANT: COCK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28217200390
CURRENT PAPLICATION NUMBER: US/11/021,441
CURRENT PAPLICATION NUMBER: US/11/021,441
FRIOR APPLICATION NUMBER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
Sequence 7, Application US/11155288

Publication No. US20060008468A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng

APPLICANT: Sinard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
TITLE OF INVENTION NUMBER: US/11/155,288
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40

SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Squence 22334, Application US/11096568A

Squence 22334, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22333, Application US/11096568A
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; ATTLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; TITLE OF INVENTION: Therby
; TITLE OF INVENTION: Therby
; TITLE OF INVENTION: US/11/096,568A
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT PILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
; LENGTH: 358
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                                                                                                                                                                                                                     Length 306;
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                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                        Score 53; DB 7;
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 7;
Pred. No. 3.1;
0; Mismatches
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i LOCATION: (1)...(358)
cother information: Ceres Seq. ID no. 12408543
US-11-096-5688-22333
                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / NAME/KEY: misc_feature
// LOCATION: (1)..(353)
/ OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
                                  TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                          71.6%;
76.9%;
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71.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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89 GVARADGPGTGAP 101
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Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity
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US-11-096-568A-22334
            LENGTH: 306
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                                                                                 FEATURE:
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US-11-096-568A-20556
US-11-096-568A-20556, Application US/11096568A
| Sequence 20556, Application US/11096568A
| Publication No. US20060048240AI
| GENERAL INPORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
| TITLE REPRENCE: Thereby
| TITLE REPRENCE: Ticol-1592PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 20556
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Sequence 496, Application US/10623155

Publication No. US20050261166A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong

APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C20

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 496

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 74; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 14; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR PILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
TYBE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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Sequence 23806 Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVERTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVERTION: Therby

TITLE REFRENCE: 2750-1592PUSZ;

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 23806

LENGTH: 134
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| LOCATION: (1):7(134)
| JOHER INDEMATION: Ceres Seq. ID no. 12415289
| US-11-096-568A-23806
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CTEULA, MACHALIA
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
; APPLICANT: MAGAHARI, YASUHIKO
TITLE OF INVENTION: NOVEL full length CDNA
TITLE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PLLING DATE: 2000-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PATENTIN VET. 2.1
; SEQ ID NO 3295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.8%; Score 46.5; D
Best Local Similarity 61.1%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches
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                                          SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, VUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 72.7
Matches 8; Conservative
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NAGAI, KEIICHI
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US-11-072-512-3295
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Sequence 22332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10542
LENGTH: 167
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      Gaps
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64.2%; Score 47.5; DB 7; Length 167;
Best Local Similarity 73.3%; Pred. No. 8.3;
Matches 11; Conservative 0; Mismatches 3; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 420;
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
| LOCATION: (1)...(420)
| JOCATION: (1)...(420)
| JOCATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332
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LOCATION: (1)..(167)

; PUTER INORWATION: Ceres Seq. ID no. 13596390

US-11-096-568A-10542
  Mismatches
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; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
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ORGANISM: Zea mays subsp. mays
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                                                                                    112 GAARGQGPGGEQPR 125
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                                          1 GAARASGPGGGAPR 14
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Best Local Similarity 71.45
Matches 10; Conservative
  10; Conservative
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US-11-096-568A-10542
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LENGTH: 420
Matches
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APPLICANT: Nycz, Jeffrey
TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
TITLE OF INVENTION: Osteoinductive Material
FILE REPRENCE: 64118.00008
CURRENT APPLICATION NUMBER: US/10/921,793
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 84
SOFFMARE: Patentin version 3.2
SEQ ID NO 38
LENGTH: 830
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TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
TITLE OF INVENTION: Osteoinductive Material
TITLE OF INVENTION: Osteoinductive Material
FILE REFERENCE: 6418.000008;
CURRENT APPLICATION NUMBER: US/10/931,198
CURRENT FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 830
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66.7%; Pred. No. 72;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 38, Application US/10931198; Publication No. US20060045902A1; GENERAL INFORMATION:
                Sequence 38, Application US/10921793
Publication No. US20060039949A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1240
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673 GSAEAAGPGAGA 684
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673 GSAEAAGPGAGA 684
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Matches 8; Conservative
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US-10-931-198-38
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Best Local Similarity
Matches 8; Conserv
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US-10-921-793-38
                                                                                                                                                                                                                                                                                                                                                     US-10-921-793-38
                                                                                                                                                                                                                                                                                                         TYPE: PRT
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27265
LENGTH: 413
                                                                                                                                                                                                         APPLICANT: Magenar, Medissa M.
APPLICANT: Magenar, Medissa M.
APPLICANT: Graziani, Edmund
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
APPLICANT: Summers, Mia
APPLICANT: Rulowski, Kerry
APPLICANT: Pong, Kevin
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
TITLE OF INVENTION: DO19/etide
FILE REPERENCE: AM-1014260S
CURRENT APPLICATION NUMBER: US 60/664,483
FRIOR FILING DATE: 2005-06-03
FRIOR PELING DATE: 2005-06-03
FRIOR PILING DATE: 2006-06-03
FRIOR PILING DATE: 2006-06-03
FRIOR APPLICATION NUMBER: US 60/576,895
FRIOR SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34
LENGTH: 280
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Pred. No. 39;
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; LOCATION: (1)...(413)
; OTHER INDEMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-2726S
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                                                                                Sequence 34, Application US/11143980
Publication No. US20050272133A1
GENERAL INFORMATION:
APPLICANT: He, Min
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Haltli, Bradley A.
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61 GVARLAGPGGRAGR 74
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Matches 9; Conservative
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ORGANISM: Streptomyces sp
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Matches 10; Conservative
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RESULT 13

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Query Match 59.5%; Score 44; DB 6; Length 298; Best Local Similarity 64.3%; Pred. No. 39; Matches 9; Conservative 0; Mismatches 5; Indels
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133 GPARPLGPGPAAPR 146
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
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ADQ18451 ADQ10446 ADS80926 ADW44353 ADY85096 ADZ28913 ADZ28913

AEA35651 ADW99402

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Human cancer antigen NY ESO-1/CAG-3 peptide.
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        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                              OM protein - protein search, using sw model
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This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CMG-3 ORF1 (see AAYO5965), a new and potent tumour antigen that is expable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAYO5967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metantasis; metanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; (USSH ) US DEPT HEALTH & HUMAN SERVICES. vaccine; cytotoxic T lymphocyte; CTL. Example 11; Page 50; 88pp; English. Cancer antigen NY ESO1/CAG-3. 98WO-US019609 97US-0061428P. Wang RF, Rosenberg SA; WPI; 1999-277270/23. WO9918206-A2 21-SEP-1998; 08-OCT-1997; 15-APR-1999. 

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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
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                                                                                                                                                                                                                                                                                         Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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                                                                                                                                                                                                              AAY05986 standard; peptide; 14 AA.
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antino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), partions of them and their cac catigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2, (see AAY05966), partions of them and their cac variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also cancer peptide animal; antisense oligonuclectides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is created by inducing cancer-specific T cells in vitro for subsequent
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                                                                               Indels
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100.0%; Score 68; DB 2;
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ive 0; Mismatches 0
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; panoreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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AAY05979 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0061428P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer antigen NY ESO1/CAG-3.
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Rosenberg SA;

Wang RF,

08-OCT-1997;

sapiens

Homo

vaccine.

Synthetic.

409918206-A2 15-APR-1999 WPI; 1999-277270/23.

The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CMG-3 (or CMG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful, as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide. Continuour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by an antibodies cancer subsequent return to a patient

Sequence 20 AA;

Gaps ö Query Match 100.0%; Score 68; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 13; Conservative 0; Mismatches 0; Indels

8 AARASGPGGGAPR 20

d

RESULT 5

AAU85105 standard; peptide; 30 AA.

AAU85105;

(first entry) Human NYNSOla segment 4. 08-MAY-2002

16-AUG-1999 (fürst entry)

AAY05979;

RESULT 4

Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immundeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.

Homo sapiens.

WO200190197-A1.

29-NOV-2001.

25-MAY-2001; 2001WO-AU000622.

26-MAY-2000; 2000AU-00007761.

(AUSU ) UNIV AUSTRALIAN NAT.

Thomson SA, Ramshaw IA;

WPI; 2002-147575/19.

N-PSDB; ABK36925

New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer. 

Example 3; Fig 27; 364pp; English.

The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides and polymucleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, coesophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence a peptide derived from a parent protein used to construct a savine of invention

Sequence 30 AA;

Gaps ; 0 100.0%; Score 68; DB 5; Length 30; 100.0%; Pred. No. 0.034; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 13; Conservative Query Match

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8

1 AARASGPGGGAPR 13

Epitope liberation-related NY-ESO-1 protein SeqID11. Lei X; Example 2; SEQ ID NO 11; 67pp; English ADK68648 standard; protein; 179 AA. Qiu Z, 07-NOV-2001; 2001US-0336968P. 07-NOV-2002; 2002US-00292413 (first entry) Diamond DC, SIMARD J J L. DIAMOND D C. WPI; 2004-167209/16. N-PSDB; ADK68674 Sequence 179 AA; US2003228634-A1. Homo sapiens. Simard JJL, 06-MAY-2004 11-DEC-2003 ADK68648; (DIAM/) (QIUZ/) (LEIX/) SIMA/) human CP 

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Best Local Similarity
                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope liberation; substrate; proteasome; cytostatic; antibacterial; protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy, neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          responses against housekeeping protéasome expressing target cells in host. The present sequence is that of a protein which is related to method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
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100.0%; Score 68; DB 8; Length 179;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                           Gaps
                                                                                                                                                                                                                                                                           Cancer associated antigen; NY-ESO-1; regression; progression; onset;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 68; DB 2; Length 180;
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                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site"
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            Pred. No. 0.16;
                           Mismatches
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                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                Cancer associated antigen NY-ESO-1.
                                                                                                                                                           AAW62584 standard; protein; 180 AA
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US016335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gure A,
                                                                                                                                                                                                                                                                                          cancer; treatment; diagnosis.
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                                                                                                                                                                                                                   (first entry)
                                                       1 AARASGPGGGAPR 13
                                                                                    49 AARASGPGGGAPR 61
                            13; Conservative
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N-PSDB; AAV38566.
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                                                                                                                                                                                                                   17-SEP-1998
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drijfhout JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1997;
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                                                                                                                                                                                        AAW62584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen Y,
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AAY05965 standard; protein; 180 AA.

RESULT 9 AAY05965 (first entry)

16-AUG-1999

AAY05965;

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The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an especific for a LAGE-1 TAP comprising contacting an isolated population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with the cytolytic T cells immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the methods and products from the present invention can be used for the methods and products from the present invention can be used for the methods and products from the present invention can be used for the methods and products from the present invention can be used for the present and a HLA present invention can be used for the products from the present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present and a HLA present invention can be used for the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders,
                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godelaine D, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 68; DB 2; Length 180; 100.0%; Pred. No. 0.16;
                                 0; Indels
     Pred. No. 0.16;
                                 Mismatches
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                                                                                                                                                                                                                                                                 AAW69665 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
100.08;
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                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1998 (first entry)
                                                                                                              50 AARASGPGGGAPR 62
                                                                                1 AARASGPGGGAPR 13
                           13; Conservative
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N-PSDB; AAV50348.
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-1998;
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                                                                                                                                                                                                                                                                                                                        AAW69665;
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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides that invention provides: vectors and host cells development of cancer. The invention provides: vectors and host cells catransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods controlly an inhibiting cancer by administering a cancer peptide, with or without an Hib Molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, cancers bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, and adenocarcinomas such as breast, prostate, ovarian, pancaetic and thyroid cancers. Malanoma is treated by inducing cancer specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                           NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; metanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; prostate pancer; pancreatic cancer; liver cancer; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                             tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
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                                                                                                                                    Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US019609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061428P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer antigen NY ESO1/CAG-3.
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX58599
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1998;
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62

50 AARASGPGGGAPR

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Gaps

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0; Indels

Mismatches

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Conservative

Local Similarity tes 13; Conserv

Matches

Query Match

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RESULT 10 AAY52430

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100.0%;
                                           .54. .162
note= "Peptide
                                                                                                                                                                                                                                                                                                                                                Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                             Chen Y,
                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                             99WO-US006875.
                                                                                                                                                                                                                          98US-00165546.
                                                                                                                                                                                                                98US-00062422
                                                                                        166
                                                                                                                             .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARASGPGGGAPR 62
                                                              .167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                  'note=
                                     note=
                                                                                                                                                                                                                                                              Jager E,
                                                                                         .28
                                                                                                                                                                                                                                                                                          2000-038483/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                       Ritter G;
                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 180 AA;
                                                                                                                                                         WO9953938-A1
                                                                                                                                                                                             24-MAR-1999;
                                                                                                                                                                                                                17-APR-1998;
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                                                                                                                                                                                                                                                               Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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        Peptide
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                                                                                                           Peptide
                                                                                                                               Peptide
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AAY70862
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/note= "Peptide presented by MHC Class I HLA-A24 and HLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Peptide presented by MHC Class I HLA-B7 and HLA-
                                                                                                                                                                                                                                                                      /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"
                                                                                                                                                                                                                                                                                                                                               34. .92
/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                                                               Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytoctoxic; helper; etimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Peptide presented by MHC Class I HLA-B44"
107. 116
/note= "Peptide presented by MHC Class I HLA-A24"
                                                                                                                                                                                                                                                                                                                             .91
.e= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                  /note= "Peptide presented by MHC Class I HLA-B44"
/note= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Peptide presented by MHC Class I HLA-B44"
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'note= "Peptide presented by MHC Class I HLA-B35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Peptide presented by MHC Class I HLA-B52"
113. .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                  .69
e= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                          .90
.e= "Peptide presented by MHC Class I HLA-Al"
                                                                                                                                                                  .53
:e= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                     .68
.e= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113. .121
/note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                  "Peptide presented by MHC Class I HLA-Al"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Peptide presented by MHC Class I HLA-A3"
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                                                                                                                                                                                                                                 "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                    "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Peptide presented by MHC Class I HLA-B8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125. .133 _ /note= "Peptide presented by
                                                                                                                                                        Location/Qualifiers
AAYS2430 standard; protein; 180 AA.
                                                             Human tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                  and HLA-B35"
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .118
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                                                                                                                                                                                                                                                              .87
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
102. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= 1
139. .1
                                                                                                                                                                                                                                                                                                                                        /note=
                                    (revised)
                                                                                                                              Homo sapiens.
Unidentified.
                                  21-OCT-2004
15-FEB-2000
                                                                                                                                                                 Peptide
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This sequence represents a human tumour antigen, NY-ESO-1, the CDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA cancer construction of the construction of construction o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                note= "Peptide (AAY52434) presented by MHC Class
.162
e= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 old LJ;
                                                                                                                                                                               "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                         presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Peptide presented by MHC Class I HLA-A3"
159. .167
note= "Peptide presented by MHC Class I HLA-A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Mismatches
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'note= "Potential O-phosphorylation site"
                                                                                                                                                                  'note= "Potential O-phosphorylation site"
                                                                                                                                                                                          /note= "Potential O-phosphorylation site"
                                                                                                                                          /note= "Potential O-phosphorylation site"
                                                                'note= "Potential N-myristoylation site"
                                                                                         'note= "Potential N-myristoylation site"
                                                                                                                                                                                                        152. .172
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                    Scanlan M, Gure AO, Chen Y, Tureci O,
                                                                                                                                                                                                                                                                                                                                                 (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC. (LUDW-) LUDWIG INST CANCER RES.
                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         96US-00725381.
                                                                                                                                                                                                                                                                                                98US-00013150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA61483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
                                                    Modified-site
                                                                            Modified-site
                                                                                                     Modified-site
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                                                                                                                                                     Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                               26-JAN-1998;
                Homo sapiens
                                                                                                                                                                                                                                                                                                                         03-OCT-1996;
                                                                                                                                                                                                                                             US6069233-A.
                                                                                                                                                                                                                                                                       30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                   old LJ;
                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF)—I that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)—recognised Antigen on MELanoma) protein, a tumour-associated antigen. The tumour-associated antigen on displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                                                                  NY-ESO-1; CAMEL, CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                     Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 68; DB 3; Length 180; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                         Klade
                                                                            Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                       Schrier PI, Aarnoudse CA, Heider K,
                                                                                                                                                                                                                                                                                   (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 62-63; 73pp; English.
AAY70862 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB03154 standard; protein; 180 AA.
                                                                                                                                                                                                                                99WO-EP007832
                                                                                                                                                                                                                                                         98EP-00119583
                                                                                                                                                                                                                                                                                               (UYHO-) UNIV HOSPITAL LEIDEN
                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-339685/29.
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD00152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eusion proteins
                                                                                                                                                                            WO200023584-A1.
                                                                                                                                                     Homo sapiens.
                                                  31-JUL-2000
                                                                                                                                                                                                                                15-OCT-1999;
                                                                                                                                                                                                                                                         16-OCT-1998;
                                                                                                                                                                                                     27-APR-2000
                         AAY70862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB03154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Sahin U, Pfreundschuh M;

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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA encoding this sequence was isolated from a cDNA carry prepared from a specimen of well-to-moderately differentiated grammous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The artigen is useful as an immunogen when combined with an adjuvant, in both protein and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to oesophageal cancer cells. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                 New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 68; DB 3; Length 180; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No.
                                                                                                                                                                                                                                                                                 Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                 e.g. infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AARASGPGGGAPR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 AARASGPGGGAPR
WPI; 2000-410880/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II; major histocompatibility complex; helper T cell; HLM-DR; cancer; muman leukocyte antigen-determining region; disease progression; disease cepression; disease onset; body tissue; body fluid; enzyme label; radioactive label; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukcoyte antigen (HLA) binding peptide, which binds to class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 68; DB 4; Length 180; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NY-ESO-1 tumour rejection antigen precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU01535 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosing testicular tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Fig 3; 50pp; English
                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                               22-JAN-2001; 2001WO-US002126.
                                                                                                                                                                                                                       22-FEB-2000; 2000US-00510635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 13; Conservative
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                                                                                                                                                                                                                                                                                                   Lethe B, Boon-Falleur
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-550091/61.
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH75118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA;
                                                                                                   WO200162917-A1
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                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                          30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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  ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining wheher a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
                                                                                                                                                           cytotoxic T cell; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scanlan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 68; DB 4; Length 180; 100.0%; Pred. No. 0.16;
                                                                                                                                                           Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotox
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcino
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 180 AA.
  AAB69946 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 3; 50pp; English
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                                                                                                                                                                                                                                                                                                                                                             14-JUL-2000; 2000WO-US019220.
                                                                                                                                                                                                                                                                                                                                                                                                     99US-00359503
                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                   Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AARASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF58634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 AA;
                                                                                                                                                                                                                                                                               WO200107917-A1
                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1999;
                                                                                                                                                                                                                                         Homo sapiens
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                                                                              27-APR-2001
                                                                                                                                                                                                                                                                                                                        01-FEB-2001
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                                       AAB69946
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Matches
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Gaps

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The sequence represents a human NY-ESO-1 tumour rejection antigen

precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to

major histocompatibility complex (MHC) Class II molecules such as human
leukocyte antigen-determining region (HLA-DR) molecules and stimulate

proliferation of helper T cells. The peptides can be administered to an
HLA-DR positive subject in order to stimulate the helper T cells. An MHC
Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
or present in free form is useful for this stimulation. The nucleic acid
is useful for screening for a cancerous condition, which involves
contacting a subject sample to a cell line transfected with the
immunoreactive cell (helper T cell), where interaction is indicative of
cancer. In addition, a sample from a patient (for example, a body fluid
or tissue) can be monitored for the amount of the complex present in the
bloodstream. This is useful for determining regression, progression or
onset of a cancerous condition. The method involves contacting the sample
with a radioactive labelled or enzyme labelled monoclonal antibody which
specifically binds with the complex
                    /note= "Phosphorylated"
                                                                                                                                                                                                                                                  Tureci O, Sahin U, Pfreundschuh M;
                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 3; 62pp; English.
                                                                                                                                   26-SEP-2000; 2000WO-US026411.
                                                                                                                                                                                                                                                                                           WPI; 2001-266156/27.
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS02254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA<sup>(</sup>;
                                                        WO200123560-A2
Modified-site
                                                                                             05-APR-2001.
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ó Query Match 100.0%; Score 68; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 13; Conservative 0; Mismatches 0; Indele

Search completed: March 13, 2006, 19:03:59 Job time: 97.8824 secs

50 AARASGPGGGAPR 62 d

A STATE OF THE STA 

Polypeptides binding to major histocompatibility complex class II human leukcyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.

1 AARASGPGGGAPR 13

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 13, 2006, 19:04:24 ; Search time 15.4471 Seconds (without alignments) 80.975 Million cell updates/sec Run on:

US-09-529-206E-28 68 Perfect score:

1 AARASGPGGGAPR 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

1: Dirl:* 2: Dir2:* 3: Dir3:* 4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	acclimation protei	H+-transporting tw	MAP kinase 3 (EC 2	CREB-binding prote		e	probable oxidoredu	hypothetical prote		Ca2+/calmodulin-de	regulatory protein	regulatory protein		hypothetical prote				Е	endopeptidase Clp	conserved hypothet	conserved hypothet	ATP dependent DNA	. steroid hormone re	hypothetical prote	hypothetical prote	flagellar basal-bo	XAA-PRO aminopepti	hypothetical prote	
П	T04476	S04673	A48082	T13828	T36874	S42585	T36115	855626	S28184	JC1451	S02165	A87431	H87399	G72663	T29031	S08341	S50754	C87425	T52451	T36104	G75580	T35694	A29345	AB2695	B97477	AB3648	F82878	T39312	T15102
DB	~	7	-	7	N	~	N	7	~	~	~	~	~	7	0	~	7	~	~	~	~	~	~				~	~	7
Length	82	286	379	3190	185	213	222	349	377	380	619	954	143	201	327	335	351	378	387	436	474	1690	521	134	134	173	357	371	389
% Query Match	64.7	64.7	64.7	64.7	63.2	63.2	63.2	63.2	63.2	63.2	63.2	•	ä	•	61.8	61.8	61.8	61.8		61.8	61.8	61.8	61.0	60.3	60.3	60.3	60.3	60.3	60.3
Score	44	44	44	44	43	43	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	41.5	41	41	41	41	41	41
Result No.	-	7	m	4	Ŋ	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

tub protein, brain	KIAA0641 protein -	DNA-invertase - Sa	hypothetical prote	glycine-rich prote	hypothetical prote	hypothetical prote	Jk-recombination s	androgen receptor	androgen receptor	androgen receptor	heterogeneous nucl	collagen alpha 1 c	tegument protein 6	hypothetical prote
S68518 A44112	T00378	JWEBT	T36712	S31415	T17265	A86182	A47214	A34721	B34721	A39248	A44192	A36226	S55659	C72683
00	1 7	н	N	-	N	~	N	~	~	N	N	~	~	7
505	1207	190	290	291	294	383	575	910	911	919	328	730	3436	103
60.3	60.3	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.8	58.1	58.1	58.1	57.4
41	41	40	40	40	40	40	40	40	40	40	39.5	39.5	39.5	39
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI00009CE5A; EMBL:X97917; NID:g1418969; P
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: blt14.2
                   C;Species: Hordeum vulgare [Darley)
C;Species: Hordeum vulgare [Darley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dinn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dinn, M.A.; Hughes, M.A.
R;Phillips, J.R.; Dinn, M.A.; Hughes, M.A.
R;Ccession: T04476
R;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-82 <PHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 2;
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%;
66.7%;
acclimation protein 2 - barley
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Best Local Similarity 66.7
Matches 8; Conservative
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1 AARASGPGGGAP 12

32 AARGAGAGGVP 43 g

H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastic to 5.0:0:117; Samma channer and the control of the control o

Gaps ö 64.7%; Score 44; DB 2; Length 286; 69.2%; Pred. No. 40; 1; Mismatches 3; Indels Query Match
Best Local Similarity 69.2'
Matches 9; Conservative

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1 AARASGPGGGAPR 13 ઠે

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Kesidues: 1-3190 <AKI>
Cross-references: UNIPROT:001368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; Pl
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A; Reference number: Z17785; MUID: 97263578; PMID: 9109493
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 2; Le
Pred. No. 3.2e+02;
1; Mismatches 1;
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Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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42;
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                                                                                                                                                                                                                                                                                            A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome: transposon Tn163
C;Superfamily: transposase repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.2%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.2%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 NGPGGGGPR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SGPGGGAPR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
                                               A;Accession: T13828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S42585
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                                                                                                                                                                                                                                                                                                             Accession More applies (EC 2.7.1.37)

C;Species: Home sapiens (man)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
N;Orcession: As8082; MUID: 93330262; PMID: 7687743
A;Reference number: A48082; MUID: 93330262; PMID: 7687743
A;Residues: 1-379 ccHa>
A;Residues: 1-379 ccMa>
A;Residues: 1-379 ccMa>
A;Residues: 14-173,'I',175-379 ccMa>
A;Reference number: 23426; MUID: 92316223; PMID: 131319925
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Aprocession: S23428
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Aprocession: S23428
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Aprocession: S23428
Aprocedule type: mRNA
Aprocession: S23428
Aprocedule type: mRNA
Aproces: UNIPARC: UPI000016A2B4; EMBL: Z11696; NID: 9228B2; PIDN: CAA77754.1; PIL
C; Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).
C; Genetics:
A; Gene: GDB: PRKM3; ERKI
A; Cross-references: GDB:135679; OMIM:601795
A; Map position: 16pter-16qter
C; Complex: monomer
C; Complex: monomer
C; Punction:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin:
A; Description: catalyzes the formation of poptidyl-serine-phosphate or peptidyl-threonin:
A; Description: Catalyzes the formation of poptidyl-serine-phosphate or peptidyl-threonin:
A; Description: Catalyzes the formation of poptidyl-serine-phosphate or peptidyl-threonine-specific C; Keywords: ATP; monomer; phosphorotein; phosphotransferase; serine/threonine-specific C; Keywords: ATP; monomer; phosphorotein; phosphotransferase; serine/threonine-specific C; Keywords: ATP; monomer; phosphotrein; protein kinase ATP-binding motif
F; 48-56/Region: protein kinase ATP-binding motif
F; 48-50
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Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
                                                                                                                                                                                                                                             N'Alternate names: extracellular signal-regulated kinase 1 (ERKI); mitogen-activated N;Contains: protein kinase (EC 2.7.1.37)
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
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CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
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Best Local Similarity 69.2
Matches 9; Conservative
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54 ASLASGOGAGAPR
                                                                                                                                                                                                          MAP kinase 3 (EC 2.7.1.-)
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A;Residues: 1-213 <ULR>
A;Cross-references: UNIPROT:Q52760; UNIPARC:UPI0000AE947; EMBL:L14931; NID:g349099; PID
A;Experimental source: strain B163N; class II transposon Th163
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-185 <MUR>
A,Cross-references: UNIPROT:098229; UNIPARC:UPI0000DB31A; EMBL:AL109848; PIDN:CAB52835
A,Experimental source: strain A3(2)
C,Genetics:
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C;Species: Rhizobium leguminosarum
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 842885
R;Ulrich, A.; Puehler, A.
Roll Gen. Genet. 242, 505-516, 1994
A;Title: The new class II transposon Th163 is plasmid-borne in two unrelated Rhizobium A;Reference number: 842584; MUID:94166763; PMID:8121409
                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SCI51.11c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: O3-Dec-1999 #text_change 09-Jul-2004 C; Daccession: T36874 B; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, August 1999 A; Reference number: Z21617 A; Accession: T36874 A; Status: preliminary; translated from GB/EMBL/DDBJ
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Length 3190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-invertase - Rhizobium leguminosarum transposon Tn163
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Gaps

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A,Molecule type: mRNA

A,Rebidues: 74-377 -CBRA

A,FCTOGB-references: UNIPARC:UPI0000023599; GB:S59517

R;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.

B;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.

B;Cc. Natl. Acad. Sci. U.S.A. 88 (8845-8849, 1991)

A;Title: Mouse Brk-1 gene product is a serine/threonine protein kinase that has the pot

A;Reference number: A41371; MUID:92020947; PMID:1717989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UP10000170C57; GB:SS8470; NID:9236372; PIDN:AAB19973.1; PID C;Superfamily: kinase-related transforming protein; protein kinase homology C;Kywords: ATP; calmodulin binding; phosphotransferase; protein kinase F;38-328/Domain: protein kinase homology <KIN: F;46-54/Region: protein kinase ATP-binding motif
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A;Residues: 1-380 cMAR>
A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:g56626; PID.
A;Experimental source: brain
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Science 249, 64-67, 1990
Affilte: An insulin-stimulated protein kinase similar to yeast kinases involved in cell A; Reference number: A35061; MUID:90312137; PMID:2164259
A; Accession: A35061
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A; Residues: 14.380 <BOUJ.
A; Cross.-Terences: UNIPARC: UP10000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID
A; Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
A; Title: Purification and properties of extracellular signal-regulated kinase 1, an inst
A; Reference number: A37140; MUID:91105092; PMID:1846291
A;Cross-references: UNIPROT:063844; UNIPARC:UPI000017558C; EMBL:214249
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse A;Reference number: A40466; MUID:91369479; PMID:1716439
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A; Residues: 43-64;167-178, XX', 180-183, XX', 185 < BO2>

A; Residues: 43-64;167-178ARC: UPI000017558F; UNIPARC: UPI0000175590

R; De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.

NA Cell Biol. 10, 505-514, 1991

A; Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse

A; Reference number: A40466; MUID: 91369479; PMID: 1716439
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NyAlternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1451; A35061; Ā37140; A40466; S24947
R;Marquardt, B.; Stabel, S.
A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
A;Feitle: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
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69.2%; Pred. No. 69;
iive 0; Mismatches
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A;Molecule type: mRNA
A;Residues: 14-94,'R',96-380 <DEM>
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A; Residues: 7-16 < CRE>
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R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S5594; MUID:95302501; PMID:7783207
A;Accession: S55626
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Scatus: Preliminary
A;Molecule type: DNA
A;Residues: 1-349 <TEL>
A;Cross-references: UNIPROT:Q66635; UNIPARC:UPI00000EDFA7; GB:U20824; NID:g695172; PIDN:A;Cross-references: Unipercore was submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
**Reference number: Z21597
**Are Generic mumber: Z21597
**Are Generic mumber: MA.*
**Are Generic T36115
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                                                                                                                                                                                                                                                                                                                     probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 32 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55626
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69.2%; Pred. No. 65;
tive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2;
Pred. No. 44;
1; Mismatches
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                                                                                                     137 AARARGRNGGAP 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARASGPSAGRP 193
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                       1 AARASGPGGGAP 12
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Best Local Similarity
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T36115
R; Murphy, L.; Harris
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61.8%;
88.9%;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity
'-ha 8; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <STO>
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A; Residues: 1-201 < KJ
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldhlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. A.G. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A87431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: L.954 <STO>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPIO00012ABED; GB:AE005673; NID:g13422833; E
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caulobacter creecentus
C;Species: Caulobacter creecentus
C;Dectes (1)-Dec-1989 #text_change 09-Jul-2004
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
B;Kaplan, J.B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A;Accession: S02164; MuID:89178645; PMID:2648000
A;Accession: S02165

A;Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA20 C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin F;41-31/Domain: protein kinase homology <KIN: F;41-31/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                              Length 380;
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Pred. No. 1.2e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                           Score 43; DB 2;
Pred. No. 70;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory protein flay - Caulobacter crescentus
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66.7%;
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66.7%;
                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                              1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AAAAPGGGGGEPR 16
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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RESULT 13

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peptidyl-tRNA hydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87399
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Luab, M.T.; DeBoy, K.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11229647
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72663
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; k
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy:
A;Reference number: A72450; MUID:99310339; PMID:10382966
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0734
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submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: 220555
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A;Molecule type: DNA
A;Residues: 1-327 <WUX>
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Pred. No. 56;
0; Mismatches
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                                                                                                                 Query Match 61.8%; Score 42; DB 2; Length 327; Best Local Similarity 72.7%; Pred. No. 85; Matches 8; Conjervative 1; Mismatches 2; Indels
A; Experimental source: strain Bristol N2; clone F53G12 C;Genetics:
A;Gene: CESP:F53G12.7
A;Map position: 1
A;Introns: 59/3; 138/1; 223/2
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Job time : 16.4471 secs
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113 AEAAGGGGGAP 123
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trypanosoma burkholderi bradyrhizob

Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 2; Length 142; 100.0%; Pred. No. 0.057; ive 0; Mismatches 0; Indels
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Last annotation update)
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15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  142 AA
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QB1VQ3 HUMAN
QB1VQ3 HUMAN
QSCX74 HUMAN
QSSQT4 HUMAN
QSB015_CRYSA
QS1415_PSEAE
Q47320_TETNG
QSKJM5_CRYNE
QSSWM1_CRYNE
Q49999_USTWA
Q4P877 9TRYP
Q633N3_BURPS
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein LAGE-2
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Q9NY13;
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NUCLEOTIDE SEQUENCE.
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CTG1B HUMAN
ID CTG1B HUMAN
AC P78358;
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   Query Match
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q96BU2_HUMAN
Q4NUK4_9DELT
Q96D18_HUMAN
Q6DHV6_HUMAN
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CTAG2 HUMAN
Q63QT8 BURPS
Q62H22 BURMA
Q96S27 HUMAN
Q6AV33 ORYSA
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063KC9 BURPS
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0528E2 ORYSA
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Nelson D.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                    Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T.;
H.AgEla, a new gene with tumor specificity.";
Int. J. Cancer 76:303-908(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                           MEDLINE=98430682; PubMed=9759882; Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.; Schwartzentruber D.J., Rosenberg S.A.; The A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames."; J. Immunol. 161:3596-3606(1998).
-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
-!- SIMILARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 1; Length 180;
Pred. No. 0.071;
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Gly-rich.
; B122C5C2C8BE1569 CRC64;
  Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997)
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100.0%; Pred. No. v.
0; Mismatches
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Name-CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ003149; CAA05908.1; -; mRNA.
AF038567; AAD05202.1; -; mRNA.
HGNC:2491; CTAGIB.
                                                                                MEDLINE=98289662; PubMed=9626360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 AA; 17992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U87459; AAB49693.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7LBY4 HUMAN PRELIMINARY;
Q7LBY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            igen; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 271:93-98(2001).
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                                       NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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                                                            rissum=Melanoma;
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=98289662; PubMed=9626360;
Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T.;
Lache B. a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
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a 35
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"Multiple pathogenic and benign genomic rearrangements occur at
kb duplication involving the NEMO and LAGE2 genes.";
Hum. Mol. Genet. 10:2557-2567(2001).
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De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
"DNA methylation is the primary silencing mechanism for a set
line- and tumor-epecific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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075638; 075637; Q9BU80; Q9U389; Q9Y479;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lethe B.G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AZ275315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
                                                                                                                                                                                                 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                  Figure M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                              Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CTAG2; Synonyms=ESO2, LAGE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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           ARG-138.

TISSUE=Placenta;

RA TISSUE=Placenta;

RA STEAUSE-CY PubMed=12477932; DOI=10.1073/pnas.242603899;

RA STEAUSE-CY R.L., Feligold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.E., Bhar N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

RA Bitschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Boak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhatesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhaterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQRPĞTPGPPPEGAQĞDGCRĞVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
R -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poly-Pro.
MSVWDQDREGAGRWRVVGWGLGSASPEGQKARDLRTPKHKV
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-18), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms=2;
Name=LAGE-1B; Synonyms=LAGE-1L;
IsoId=075638-1L; Sequence=1soplayed;
Name=LAGE-1A; Synonyms=LAGE-1S;
IsoId=075638-2; Sequence=1XSP 004301;
TISSUE SPECIFICITY: Testis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, pon-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
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/FTId=VAR_007857.
8BE0EE00AR55E8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
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/FTId=VAR_007855.
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/FTId=VAR_007856.
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EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, BC002835; CAA10194.1; -; mRNA.
EMBL; BC002833; AAH02831.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          head and neck cancers.
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188
210
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Best Local Similarity
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STATISTICATION DOI: 10.1073/pnas.0403302101;

BubMed=15377794; DOI=10.1073/pnas.0403302101;

Atkins T., Croseman L.C., Pitt T., Churcher C., Mungall K.L.,

Bentley S.D., Sebainia M., Thomson N.R., Bason N., Beacham I.R.,

Bentley S.D., Sebainia M., Thomson N.R., Bason N., Deacham I.R.,

And Chilliagworth T., Crohin A., Crosestt B., Davis P., DeShazer D.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Songsivilai S., Stevens K., Tumapas S., Vesaratchavest M.,

Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

Genomic plasticity of the causative agent of melioidosis,

Burkholderia pseudomallei.";

Droc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

REMBL, BRST1965; CAHSG461; -; Genomic DNA.

GO; GO:0003897; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0005860; P:DNA replication; IEA.

InterPro; IPR010122; DNA polifil delta.

REPROS. TIGR01128; hold; 1.
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                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
NCBI_TaxID=28450;
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Burkholderiaceae, Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC 23344;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 2; Length 362;
Pred. No. 13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                      Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7)
Name-hold, OrderedLocusNames=BMA2451;
Burkholderia mallei (Pseudomonas mallei).
                                                                                                                   362 AA
                                                                                                                     PRT;
                                                                                                                                                       Created)
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                                                                                                                 QG3QT8 BURPS PRELIMINARY;
Q63QT8;
1 AARASGPGGGAPR 13
                              50 AARASGPRGGAPR 62
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Q62H22_BURMA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 ARAAGPGGDAPR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 STRAIN=K96243;
                                                                                                     SURPS
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Gaps

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1; Indels

0; Mismatches

Conservative

Matches

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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002),
           Hypothetical protein OSJNBa0063J18.9
                                                       Name=OSJNBa0063J18.9;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. Uls. A. 101:14246-14251 (2004).
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Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
Higgs D.R.;
"Sequence and pathology of the fully annotated terminal
Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
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                                                                                                                                                                                                                                                                                                                                                                               G1.60 prints 231; ...
G1.60 prints 231; ...
G2.60 prints 231; ...
G2.60 prints 231; ...
G3.60 prints 231; ...
G4.60 prints 231; ...
G5.60 prints 231; ...
G6.60 prints 231; ...
G7.60 prints 231; ...
G8.60 prints 231; ...

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Pred. No. 13;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome, Nucleotidyltransferase, Transferase. SEQUENCE 362 AA, 38726 MW, D5FP3DE783D41E41 CRC64;
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SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;
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Last annotation update)
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Ensembl; ENSG00000167933; Homo sapiens.
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QEAV33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AARASGPGGGAPR 13
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Matches 10; Conserv
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ID Q67
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                     Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hasiao J., Blunt S., Vanaken S.S., Ricdmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., "", Quackenbush J., Churza sativa chromosome 3 BAC OSJUBBOGGJJB genomic sequence.", Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypochetical protein.
SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
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Last annotation update)
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76.9%;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Stuller G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hasieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., & Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., & Bras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., & Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., & Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fathon E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Brinerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Director MGC Project;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013422; AAH13426.1; -; mRNA.
SEQUENCE 896 AA, 94247 MW; ODE6869BCFD4C471 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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QCDHVG;
25-OCT-2004 (TEMBLE1. 28,
25-OCT-2004 (TEMBLE1. 28,
25-OCT-2004 (TEMBLE1. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLEKHG2 protein (Fragment).
Name=PLEKHG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-2CP-C;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dehalogenans 2CP-C.";
Submitted (JUN-2005) to the BMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=AdehDRAFT_2813;
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter"
                                                                                                                                                                                                                                                                            Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 895;
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76.9%; Pred. No. 1.18+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                      Indels
                   NUCLEOTIDE SEQUENCE.

TISSUB=Pancreas;

Director MGC Project;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, BC015174; AAH15174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                        Score 50; DB
Pred. No. 26;
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                                                                                                                                                                                                                                                                     73.5%;
81.8%;
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01-DEC-2001 (TrEMBLrel. 19, L,
01-DEC-2001 (TrEMBLrel. 19, L,
PLEKHG2 protein.
Name=PLEKHG2,
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           797 ARRARGAGGAPR 809
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Q96D18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4NUK4 9DELT PRELIMINARY;
Q4NUK4;
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                                                                                                                                                                                                                                                                                                                                      9; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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13-SEP-2005
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Q96D18_HUN
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Gaps

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-1- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
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PubMed=14702039; DOI=10.1038/ng1285;

PubMed=14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishi S.,

Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Sugawara M., Takahashi M., Kantau K., Yokoi T., Furuya T., Kikkawa E.,

Amazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

Pujimori K., Tanai H., Kimta M., Watanabe N., Hiracka S.,

Rujimori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

Imose N., Masashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,

Nomikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 2; Length 1253;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                               Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 PH domain.
InterPro; IPRO01849; PH.
InterPro; IPRO01849; PH.
InterPro; IPRO0189; Ph.OGBF.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
SWART; SW00133; PH; 1.
SWART; SW00135; RhoGEF: 1.
SWART; PSS0010; DH 2; 1.
PROSITE; PSS0001; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                         1253 AA; 134404 MW; 534EB31283E535C5 CRC64;
                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FLJ00018 protein (Fragment).
Name=PLEKHG2; Synonyms=FLJ00018;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1430 AA.
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                         TISSUE=Pancreas;
Director MGC Project;
                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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PACA CHICK STANDARD, PRT; 175 AA.
P41534; 053WW0;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Glucagon-family neuropeptides precursor [Contains: Growth hormone-releasing factor 1-6 (GRP) (Growth hormone-releasing factor 1-6 (GRP) (Growth hormone-releasing hormone) (GHRH); Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
(PACAP27); Pituitary adenylate cyclase activating polypeptide-38
(PACAP-38) (PACAP-38)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]

NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].

MEDLINE=97174314; PubMed=9022048;

MCRORY J.E., Parker R.L., Sherwood N.M.;

MCRORY J.E., Parker R.L., Sherwood N.M.;

"Expression and alternative processing of a chicken gene encoding both growth hormone—releasing hormone and pituitary adenylate cyclase—
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Pujiwara T., Pujiwara T., Pujiwara T., Pujiwara T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Okitani R., Kawakami T., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura Y., Okara O., Isogai T., Sugano S., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 131-168.
Yasubara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
Yasubara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
"Isolation and primary structure of chicken PACAP.";
Regul. Pept. 37:326-326(1992).
-!- FUNCTION: Primary role of GRP is to release GH from the pituitary.
-!- FUNCTION: PACAP plays pivotal roles as a neurotransmitter and/or a neuromodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 2; Length 143
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1430 AA; 152528 MW; E4DF0BFDACCB6A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG00000090924; Homo Bapiens.
HGNC; HGNC:29515; PLEKHG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 36:40-45(2004).
-!- SMILARITY: Contains 1 PH domain.
EMBL; AK024429; BAB15719.1; -; mRNA.
HSSP; Q64096; 1KZ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activating polypeptide.";
DNA Cell Biol. 16:95-102(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335 ARROGPGGGAP 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
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Gaps
         "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism."; Nucleic Acids Res. 32:4937-4944(2004).
                                                                                                                         EMBL, AP006646; BAD40403.1; -; Genomic DNA.
GO; GO:0004665; F.prephenate dehydrogenase (NADP+) activity; IEA.
GO; GO:0006671; P:tyrosine biosynthesis; IEA.
Interpro; IPR003099; Prephen_dehydrog.
Pfam; PF02153; PBH; 1.
Complete protecome.
SEQUENCE 322 AA; 32843 MW; 09A06ACOAFA734EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; Score 49; DB 2; Length 322; 90.9%; Pred. No. 58; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 13, 2006, 19:14:27 Job time: 94.3647 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AARASGPGGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AADASGPGGGA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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PEAM: PR00123; Hormone 2; 2.
PRINTS; PR00275; GLUCAGON.
PROSITE; PS00260; GLUCAGON: 2.
Alternative splicing; Amidation; Cleavage on pair of basic residues; Blicet protein sequencing; Glucagon family; Hormone; Signal.
1 23 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucine amide (G-158 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lysine amide (G-169 provides amide
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RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG
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PubMed=15383646; DOI=10.1093/nar/gkh830;
Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform GRF 33-46).
/FTd=vSp 001759.
Missing (In isoform GRP 1-43)
/FTtd=vSP 001760.
0DB54995F0AA9DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 1; Length 175;
Pred. No. 33;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Prephenate dehydrogenase.
                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                     IsoId=P41534-3; Sequence=VSP_001759;
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide-27
                                                                                                                                                                                                                    IsoId=P41534-2; Sequence=VSP_001760;
                                                                                 Name=GRF 1-46;
IsoId=P41534-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U71184; AAB51200.1; -; mRNA.
EMBL; U71184; AAB51201.1; -; mRNA.
EMBL; U71185; AAB51202.1; -; mRNA.
EMBL; U67275; AAC64494.1; -; Genomic_DNA.
HSSP; P18509; IGEA.
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Symbiobacterium thermophilum
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Q67PJO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AARASGPGGGAPR 13
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ALTERNATIVE PRODUCTS
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168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                       Name=GRF 1-43;
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MOD_RES
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067PJ0 SYM
1D C67PJ
AC Q67PJ
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23, Appl 23, Appl 23, Appl 283, Appl 283, Appl 25, Appl 14, Appl 14, Appl

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US-09-252-991A-27111

US-09-902-540-12383

US-09-902-540-12383

US-09-861-012A-23

US-09-861-012A-23

US-09-861-090A-23

US-09-861-090A-23

US-09-861-097-23

US-09-252-991A-28380

US-09-252-991A-28380

US-09-252-991A-28380

US-09-252-901A-28380

US-09-55-80-25

US-09-411-628-14

US-09-538-092-1021

US-09-538-092-1021

US-09-642-749-25

US-08-417-197-39

US-08-938-291A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leth, Bernard
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Palleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02210

ZIP: 02210

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                              US-09-270-767-59895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Ameterdam, John R.
REGISTRATION NUMBER: 40,212
REPERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-720-3500
TELEPAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; FL.
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Best Local Similarity 100.
Matches 13; Conservative
  MOLECULE TYPE: protein US-08-791-495-9
  STREET: 600 A
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    STATE:
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Sequence 8, Appli
Sequence 25, Appli
Sequence 15, Appli
Sequence 17, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 17, Appli
Sequence 1749, Appli
Sequence 10, Appli
Sequence 7, Appli
Sequence 17, Appli
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Sequence 117, Appli
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Sequence 31759, A
Sequence 20577, A
Sequence 24923, A
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Sequence 30527, A
Sequence 32326, A
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Sequence 29442, A
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                                                                                                                            March 13, 2006, 19:14:49; Search time 24.1647 Seconds (without alignments) 44.477 Million cell updates/sec
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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
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US-08-937-263B-8
US-09-392-714-28
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US-09-341-829A-9
US-09-341-829A-9
US-09-341-829A-7
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                                                                                                                                                                                                                                                                                                                                               572060 segs, 82675679 residues
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                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                              1 AARASGPGGGAPR 13
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Maximum DB seq length: 200000000
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APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knutch, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COMPUTER READABLE FORM:

MEDIION TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT: October 3, 1996
ATTORNEY/AGENT OCTOBER: 40,177
REFERENCE/DOCKET NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMULICATION INPORMATION:
TELECOMMULICATION NUMBER: 10,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMULICATION INPORMATION:
TELECOMMULICATION NUMBER: 10,177
REFERENCE/DOCKET NUMBER: 10,177
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Patent No. 6525177
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-751-798-8
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100.0%; Pred. No. 0.068;
tive 0; Mismatches 0; Indels
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US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 6666147

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
FILE REFREENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
COUNTY.
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
                                                                                        OPERATING SYSTEM: FC.L...
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
APPLICATION NUMBER: 09/062,422
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6525177man D. REGISTRATION NUMBER: 30,946
TELECHONEY/ACET NUMBER: LUD 5466.
TELECHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEGUENCE CHARACTERISTICS:
LENGTH: 180
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-392-714-25
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    <151> 1998-01-27
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 0.068;
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APPLICANT: Leth , Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/1105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenfield & Sacks, P.C.
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 180
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; Sequence 30, Application US/09849602
; Patent No. 6794501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Wolf, Greenfield
600 Atlantic Avenue
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                               Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-341-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserval
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 30
                                                                                                                    TYPE: PRT
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                                                                                                             APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Sure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
USES THEREOF
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COMPUTER: IBM

COMPUTER: IBM

COMPUTER: IBM

CORPATING SYSTEM: PC-DOS

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION DATA:

RAPLICATION DATE: 09/062,422

FILING DATE: 09/062,422

FILING DATE: 09/061,233

APPLICATION NUMBER: 09/062,422

FILING DATE: APPLICATION NUMBER: 09/062,422

FILING DATE: APPLICATION NUMBER: 09/062,422

FILING DATE: September 15, 1997

APPLICATION NUMBER: US 08/725,182

RILING DATE: September 15, 1997

APPLICATION NUMBER: US 08/725,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <151> 1997-01-27
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 68; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 0.068; Matches 13; Conservative 0; Mismatches 0; Indels
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APPLICANT: Leth,, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Good-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Pifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. 6723832man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
                                            Sequence 15, Application US/09165546D Patent No. 6723832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09341829A
Patent No. 6794131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 180 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                      US-09-165-546D-15
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TYPE: PRT
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APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
APPLICANT: Godelaine, Daniele
CURRENT APPLICATION NUMBER: US /09/341,829A
CURRENT PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DS 08/791,495
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
TOWN OF THE CONTRACT O
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Pred. No. 0.75;
0; Mismatches 1; Indels
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88.2%; Score 60; DB 2; Length 180;
Best Local Similarity 92.3%; Pred. No. 0.75;
Matches 12; Conservative 0; Mismatches 1; Indels
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US-08-791-495-5
; Sequence 5, Application US/08791495
; Fatent No. 5811519
; GENERAL INFORMATION:
APPLICANT: Locab, Sophie
APPLICANT: Lucab, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TILLE OF INVENTION:
APPLICANT: Boon-Falleur, Thierry
TILLE OF INVENTION: Lill TUMOR SPECIFIC GENES
CORRESPONDENCE ADDRESS:
                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-3500
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09341829A Patent No. 6794131 GENERAL INFORMATION:
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Best Local Similarity 92.3%;
Matches 12; Conservative
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TYPE: amino acid
TOPOLOGY: limear
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Pred. No. 0.86;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%; Score 60; DB 2; Length 210; 92.3%; Pred. No. 0.86; tive 0; Mismatches 1; Indels
                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                          L0461/7005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-341-829A-5; Sequence 5, Application US/09341829A; Patent No. 6794131
                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELEPOMONICATION INFORMATION:
TELEPOMONE: 617-720-350
TELEPHONE: 617-720-3441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%;
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 210 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AARASGPGGGAPR 13
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12, Conservative
                                                                        ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-341-829A-5
                                                               USA
             STREET: 600 A
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LENGTH: 210
                                                               COUNTRY:
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Gaps
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                                                                                                                    Length 143;
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                                                                                                                                                                                                  Indels
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Sequence 7, Application US/08789329C
Sequence 7, Application US/08789329C
Sequence 7, Application US/08789329C
SECRETAL INFORMATION:
APPLICANT: SHERWOOD ET AL.
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL.
TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Klarquiet Sparkman Campbell Leigh & ADDRESSEE: Klarquiet Sparkman Campbell Leigh & ADDRESSEE: Whinston, LLP STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: 121 S.W. Salmon Street STREET: 121 S.W. Salmon Street STREET: Suite 1600 CITY: Portland STATE: Oregon COUNTRY: United States of America ZIP: 97204-2988 COMPUTER READABLE FORM: Windows NT SOFTWARE: WordPerfect 7.0 & ASCII CURRENT APPLICATION NATA: APPLICATION NATA: APPLICATION NUMBER: US/08/789,329C FILING APPLICATION NUMBER: US/08/789,329C FILING APPLICATION NUMBER: PRILING APPLICATION PRILING APPLICATION PRILING APPLICATION NUMBER: PRILING APPLICATION PRILING APPLICATION PRILING APPLICATION PRILING APPLICATION PRILING APPLICATION PRILING APPLICATION PRILING APPL
                                                                                                                    Score 49; DB 2;
Pred. No. 16;
0; Mismatches
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; Sequence 3, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
APPLICANT: SHERWOOD ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Barp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                        72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 172 aa
                                                                                                                                                                                                                                                                             1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                            54 ALRAGAPGGGGPR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AARASGPGGGAPR 13
                                                                                                                    Query Match 72.1
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ALRAGAPGGGGPR 66
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Matches 9; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-789-329C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-789-329C-7
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    Sequence 17249, Application US/09252991A

Sequence 17249, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17249

LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-08-789-329C-10

US-08-789-329C-10

Sequence 10, Application US/08789329C

Patent No. 6165755

GENERAL INFORMATION:

TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL

TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL

TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL

TITLE OF INVENTION: POR IMPROVED POULTRY PRODUCTION

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Whinsten, LL

STREET: One World Trade Center

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600

CITY: World Content

STATE: Oregon

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER SEADABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER: Worlderfect 7.0 & ASCII

CURRENT APPLICATION UNBER:

PRIDA APPLICATION NUMBER:

STING DATE:

APPLICATION NUMBER:

PRIDA APPLICATION NUMBER:

PRIPA APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%; Score 50; DB 2; Length 160; 69.2%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
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REGISTRATION NUMBER: 41,401
REFERENCEDOCKET NUMBER: 2847-46468/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEPAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AGRRAGEGGSAPR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.5
Best Local Similarity 69.2
Matches 9; Conservative
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TYPE: amino acid
STRANDEDNESS: single
US-09-252-991A-17249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-17249
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TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
TITLE OF INVENTION: CRI IMPROVED FOULTRY PRODUCTION
OWRRESPENCES. 20
CORRESSEE: Winston. Lib.
ADDRESSEE: Winston. Lib.
ADDRESSEE: Winston. Lib.
STREET: 0.0 world Tada Center
STREET: 0.12 s.w. Salmon Street
STREET: 0.12 s.w. Salmon St
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Search completed: March 13, 2006, 19:18:51 Job time: 24.1647 secs

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1 AARASGPGGGAPR 13
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CORGANISM: Homo sapiens
US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
 US-10-296-734-1404
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LENGTH: 30
 TYPE: PRT
80010EEEEEEEE
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Sequence 7, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1404, Ap
Sequence 202, App
Sequence 8, Appli
Sequence 30, Appli
Sequence 8, Appli
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Sequence 1454, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           March 13, 2006, 19:51:56 ; Search time 78.6118 Seconds (without alignments) 69.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 386, Sequence 832, Sequence 139, Sequence 11, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 71, A Sequence 14, A Sequence 3, Ap Sequence 74, A
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                       Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: 'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-296-734-1404
US-10-482-029-202
US-09-849-602-30
US-09-849-602-30
US-10-021-182-8
US-10-207-655-71
US-10-204-614-14
US-10-205-027-386
US-10-296-734-832
US-10-296-734-832
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US-10-296-734-832
US-10-657-022-74
US-10-657-022-74
US-10-657-022-74
US-10-677-03-11
US-10-877-373-9
US-11-067-064-74
US-11-067-064-74
US-11-067-059-74
US-11-11-144-912-27
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                 1 AARASGPGGGAPR 13
                                                                                                                      US-09-529-206E-28
68
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                          Database
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
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75, Appl
834, App
834, Appl
75, Appli
75, Appli
76, Appl
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                                                                                                                                                                                                            Sequence Seq
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US-10-296-734-1436
US-10-298-027-388
US-10-188-832-141
US-10-146-473-69
US-10-17-937-75
US-10-26-734-834
US-10-26-734-834
US-10-26-734-834
US-10-67-02-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-75
US-11-67-15-76
US-11-67-15-76
US-11-67-15-76
US-11-67-16-76
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ALIGNMENTS

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Gaps
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Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, lan A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 100.0%; Score 68; DB 4; Length 30; Similarity 100.0%; Pred. No. 0.076; 13; Conservative 0; Mismatches 0; Indels
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7 AARASGPGGGAPR 19

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US-10-422 Sequence 202, Application US/10482029 Sequence 202, Application US/10482029 Publication No. US20050037445A1 GENERAL INFORMATION: Oncology drug innovation FILE REFERENCE: P 573 PC00 CURRENT APPLICATION NUMBER: US/10/482,029 CURRENT PILING DATE: 2003-12-29 NUMBER OF SEQ ID NOS: 437 SEQ ID NO 202 LENGTH: 179

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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-teeng; Scanlan, Matthew;
APPLICANT: Chen, Yao-teeng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STREET: New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Query Match 100.0%; Score 68; DB 5; Length 179; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 3; Length 180;
Pred. No. 0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. US20020010321Alman
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: OCLOBER 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                 Sequence 8, Application US/09751798
Patent No. US20020610321A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                 1 AARASGPGGGAPR 13
                                                                                                                                              50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AARASGPGGGAPR 62
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TOPOLOGY: linear
                                                                                                                                                                                                                  RESULT 3
US-09-751-798-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-751-798-8
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RESULT 4
US-05-849-602-30
US-05-849-602-30
Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Mathew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 3; Length 180; 100.0%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
CITY: New York
COUNTRY: USA
ZIP: 10103
COMPUTER NEADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 0.37; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, No. US20020164665Alman D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
               APPLICANT: Chen, Yao-Teeng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: LO461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: «Unknown-
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8, Application US/10023182; Publication No. US20020164665Al
Stockert, Elisabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AARASGPGGGAPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-849-602-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-023-182-8
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Gaps
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100.0%; Pred. No. 0.37;
Live 0; Mismatches 0; Indels
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                             | GENERAL INFORMATION: |
| APPLICANT: Simard, John J. L. |
| APPLICANT: Simard, David C. |
| APPLICANT: Simard, David C. |
| TITLE OF INVENTION: EPITOBE SYNCHRONIZATION IN ANTIGEN |
| TITLE OF INVENTION: PRESENTING CELLS |
| FILE REFERENCE: CTLIAM. 21CFLC |
| CURRENT PAPLICATION NUMBER: US/10/026,066 |
| CURRENT PAPLICATION NUMBER: 09/561,074 |
| PRIOR FILING DATE: 2000-04-28 |
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1 Sequence 74, Application US/10117937

2 Sequence 74, Application US/10117937

3 Fublication No. US2003022029A1

3 GENERAL INFORMATION:

4 APPLICANT: CIL IMMUNO THERAPIES CORP.

5 APPLICANT: DIAMOND, David, C.

6 APPLICANT: DIAMOND, David, C.

7 APPLICANT: LIU, Liping

8 APPLICANT: LIU, Liping

9 TITLE OF INVENTION: EPITOPE SEQUENCES

17 TILE OF INVENTION: EPITOPE SEQUENCES

18 TILE REPERENCE: CTLIMM.027A

19 CURRENT APPLICATION NUMBER: US 60/282,211

19 PRIOR FILING DATE: 2001-04-06

19 PRIOR FILING DATE: 2001-11-07

19 PRIOR FILING DATE: 2001-11-07

19 PRIOR FILING DATE: 2001-11-07

10 PRIOR SEQ ID NOS: 602

10 NUMBER OF SEQ ID NOS: 602
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Best Local Similarity 100.'
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Matches 13; Conservative
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US-10-117-937-74
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Publication No. US20030175250A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOGER, Elke
APPLICANT: OLD, Lloyd
APPLICANT: APPLICANT: USOLATED
APPLICANT: OLD, Lloyd
APPLICANT
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APPLICANT: Ledbetter, Martha S.

TITLE OF INVENTINE DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT PILING DATE: 2002-07,655

CURRENT FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOFTWARE: Patentin version 3.0
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        100.0%; Score 68; DB 4; Length 180; 100.0%; Pred. No. 0.37; ative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.37;
tive 0; Mismatches 0; Indels
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; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
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10S-10-026-066-3
5 Sequence 3, Application US/10026066
7 Publication No. US20030215425A1
Query Match
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-207-655-71
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LENGTH: 180
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US-10-777-053-11
LENGTH: 180
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                                                                                                                         APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Glanberg, Wendy M.
APPLICANT: Glanberg, Wendy M.
APPLICANT: Glanberg, Wendy M.
APPLICANT: Glanberg, Wendy M.
APPLICANT: Glanberg, Rechard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Watson, Susan R.
APPLICANT: Watson Statement R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson R.
APPLI
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NUMBER OF SEQ ID NOS: 1386
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Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR PILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 832
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Matches 13; Conservative 0; Mismatches
                           Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 139, Application US/10188832

Sequence 139, Application US/10188832

Publication No. US20040076955A1

GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Matasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE OF INVENTION: Cancer
CURRENT APPLICATION NUMBER: US 60/302,814

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 60/313,705

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-13
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Publication No. US2004013208BA1

GENERAL INFORMATION:

APPLICANT: Diamond, David C.

CURRENT APPLICATION NUMBER: US/10/777,053

CURRENT FILING DATE: 2004-02-10

PRIOR FILING DATE: 2002-11-07
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                                                                                                                                                                                                                                     Query Match 100.0%; Score 68; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                    ; OTHER INFORMATION: NYNSO1a consensus polypeptide US-10-296-734-832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AARASGPGGGAPR 62
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-188-832-139
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Gaps
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                                                                                                                                                                                                                     RESULT 15
US-10-657-022-74

| Sequence 74, Application US/10657022
| Publication No. US20040180354A1
| GENERAL INFORMATION:
| APPLICANT: Simard, John J. L. |
| APPLICANT: Diamond, David C. |
| APPLICANT: Liu, Liping |
| TILLE OF INVENTION: BETTOPE SEQUENCES |
| TILLE REFERENCE: MANNK. 032A |
| CURRENT APPLICATION NUMBER: 06/409123 |
| PRIOR APPLICATION NUMBER: 60/409123 |
| PRIOR APPLICATION NUMBER: 60/
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                                                           1 AARASGPGGGAPR 13
                                                                                                                           50 AARASGPGGGAPR 62
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-657-022-74
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Gure, Ali, Old, Lloyd, Ritter, Gerd
Gure, Ali, Old, Eloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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CORRESPONDENCE ADDRESS:
ADDRESSES: FULBRICHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: US/09/165,546D
FILING DATE: April 17, 1998
APPLICATION NUMBER: US/09/165,546D
FILING DATE: SEQUENDER 15, 1997
APPLICATION NUMBER: US/09/125,182
FILING DATE: SEQUENDER 15, 1997
APPLICATION NUMBER: US/09/125,182
FILING DATE: SEQUENDER 15, 1996
APPLICATION NUMBER: US/08/725,182
FILING DATE: COCCOBER 3, 1996
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REGISTRATION NUMBER: 30, 946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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100.0%; Score 68;
Best Local Similarity 100.0%; Pred. No. '
Matches 13; Conservative 0; Mismatch
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-10-751-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AARASGPGGGAPR 13
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapien
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Tue Mar 14 10:35:58 2006
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March 13, 2006, 19:54:06; Search time 8.87059 Seconds (without alignments) 40.793 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpāa/US08_NEW PUB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/US10 NEW_PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/US11 NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapob 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

uc	7, Appli	28, Appl			22334, A	22333, A	22332, A	23806, A	3295, Ap	16, Appl			272		2304	10542, A	-			58,	2,	33	99	34,	376
Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΩI	US-11-155-288-7	US-11-021-441-28	US-10-623-155-496	US-11-096-568A-20556	US-11-096-568A-22334	US-11-096-568A-22333	US-11-096-568A-22332	US-11-096-568A-23806	US-11-072-512-3295	US-11-109-156-16	US-11-096-568A-26217	US-10-531-036-35	US-11-096-568A-27265	US-11-096-568A-641	US-11-096-568A-23045	US-11-096-568A-10542	US-11-110-424-4	US-11-087-099-6009	US-11-100-640-26	US-11-108-528-58	US-11-179-958A-2	US-11-072-512-3369	US-11-037-243-66	US-11-143-980-34	US-11-087-099-3763
80	7	7	y	7	7	7	7	7	7	7	7	9	7	7	7	7	7	7	7	7	7	^	7	7	7
% Query Match Length DB	180	240	20	306	353	358	420	134	678	379	558	974	413	162	249	167	119	268	306	365	537	555	953	280	291
% Query Match	100.0	100.0	82.4	69.1	69.1	69.1	69 ii	67.6	66.2	64.7	64.7	64.7	63.2	61.8	61.8	61.0	60.3	60.3	60.3	60.3	60.3	60.3	60.3	59.6	58.8
Score	89	9	26	47	47	47	47	46	45	44	44	44	43	42	42	41.5	41	41	41	41	41	41	41	40.5	40
Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 7762, Ap Sequence 2721, Ap Sequence 2722, Ap Sequence 22508, A Sequence 11286, A Sequence 11286, A Sequence 54, Appli Sequence 18222, A Sequence 18222, A Sequence 18222, A Sequence 18222, A Sequence 18221, A Sequence 18221, A Sequence 18, Appl	Sequence 11, Appl Sequence 38, Appl Sequence 38, Appl
US-11-087-099-7762 US-11-096-568A-20715 US-11-096-568A-22508 US-11-240-769-58 US-11-240-769-58 US-11-240-769-58 US-11-240-769-58 US-110-234-1240 US-11-239-57-8 US-11-239-54-4 US-11-096-568A-18223 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-096-568A-18221 US-11-076-758A-1821 US-11-076-758A-1821 US-11-076-758A-1821 US-11-076-758A-1821 US-11-076-758A-1821 US-11-076-758A-1821 US-11-076-758A-1821	US-11-078-189-11 US-10-921-793-38 US-10-931-198-38
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1832 178 213 223 238 238 238 430 430 430 440 496 618 618 618	736 830 830
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## ALIGNMENTS

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Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DURENSKY, Thomas W., Jr.
APPLICANT: DUKENSKY, Thiliam S., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT PLING DATE: 2004-12-23
FRIOR PILING DATE: 2004-10-06
             Sequence 7, Application US/11155288
Publication No. US20060008468A1
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTICENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REPRENCE: MANNK. 050A
CURRENT APPLICATION NUMBER: 05/506.969
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR FILING DATE: 2004-06-17
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
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CRGANISM: Homo sapiens
US-11-155-288-7
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US-11-021-441-28
US-11-155-288-7
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Gaps

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US-11-096-568A-22334
US-11-096-568A-22334
Sequence 22334, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORWATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: US/11/096,568A
CURRENT APPLICATION UNDMER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22334
LENGTH: 353
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Sequence 2233, Application US/11096568A
Sequence 2233, Application US/11096568A
Sequence 2233, Application US/11096568A
Sequence 2233, Application US/11096568A
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22333
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                                                                                                                                                                                                             Length 306;
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                                                                                                                                                                                                                                                                2; Indels
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Pred. No. 13;
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                                                                                              NAME/KEY: misc_feature
| LOCATION: (1)..(306)
| OTHER INDEMATION: Geres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                               Score 47; DB 7
Pred. No. 11;
0; Mismatches
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; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays subsp. mays
                               TYPE: PRT ORGANISM: Zea mays subsp. mays
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: LOCATION: (1). (1558)

: OTHER INFORMATION: Ceres Seq.

US-11-096-568A-22333
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69.2%;
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81.8%;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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                                                                                                                                                                                            Query Match
Best Local Similarity 81.0-
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AARASGPGGGAPR 13
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                                                                                                                                                                                                                                                                                                                                                       91 ARADGPGTGAP 101
                                                                                                                                                                                                                                                                                                              2 ARASGPGGGAP 12
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Best Local Similarity
         LENGTH: 306
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US-11-096-568A-20556
US-11-096-568A-20556
Sequence 20556, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Publication No. US20050261166A1
GENERAL INPORMATION:
APPLICANT: Weng, Tongtong
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 68; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR PILING DATE: 2004-06-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR PILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
SOFTWARE: PSECS OF WINDOWS VERSION 4.0
SOFTWARE: PSECS OF WINDOWS VERSION 4.0
ENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 AARASGĘGGGAPR 122
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-623-155-496
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APPLICANT: Jun-Ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 7; Length 678;
Pred. No. 41;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                           APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MASUHO, YASTHIKO
TITLE OF INVENTION: NOVEL Full length cDNA
FILER REFERENCE: 084335-0191
CURRENT FILING DATE: 2005-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 6/350,978

PRIOR PILING DATE: 2002-03-07

PRIOR PILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: UP 2001-379298

PRIOR PILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SQFTWARE: PatentIn Ver. 2.1

FRANCE OF SEQ 10 NOS: 4096
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CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
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PRIOR FILING DATE: 2002-01-29
PRIOR PPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
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US-11-109-156-16
Self Application US/11109156
Publication No. US20050250144A1
GENERAL INFORMATION:
                ISOGAI, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                                  ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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80.0%;
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Jun-Ichi Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shizuko Ishii
Tomoyasu Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.v
                                                                                                                                                                                                   OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                            IRIE, RYOTARO
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APPLICANT:
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Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22332
LENGTH: 420
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 23806
LENGTH: 134
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: misc_feature
| LOCATION: (1)...(420)
| JOCHER INFORMATION: Ceres Seq. ID no. 12408542
| US-11-096-568A-22332
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i LOCATION: (1)..(134)
corner INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-5688-23806
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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ORGANISM: Zea mays subsp. mays
                                                                            113 AARGQGPGGEQPR 125
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                                       1 AARASGPGGGAPR 13
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Matches 9; Conservative
  9; Conservative
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69 ARGAGPGAGAP 79
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Best Local Similarity 7
                                                                                                                                                           US-11-096-568A-22332
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Matches
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US-11-096-568A-27265

Sequence 27265, Application US/11096568A

Sequence 27265, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

LENGTH: 413
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US-11-096-568A-641

Sequence 641, Application US/11096568A

Fublication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

APPLICANT: Alexandrov, Nickolai et al.

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT APPLICATION NUMBER: 2005-04-01

NUMBER: OF SEQ ID NOS: 34471

SEQ ID NO 641
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Pred. No. 49;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Length 974;
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LOCATION: (1). (413)
OTHER INFORMATION: Ceres Seq. ID no. 15180691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 44; DB 6
; Pred. No. 76;
0; Mismatches
   PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: EP 02024747.4
PRIOR APPLICATION NUMBER: EP 02023560.2
PRIOR FILING DATE: 2002-11-06
PRIOR FILING DATE: 2002-10-22
PRIOR PLING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: EP 02022880.5
PRIOR APPLICATION NUMBER: BO 20022880.5
NUMBER OF SEQ ID NOS: 3.7
SOOTWARE: PATENTIN VERSION 3.3
SEQ ID NO 3.5
LENGTH: 974
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ORGANIZM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 71.4%;
Matches 10; Conservative
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US-10-531-036-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
. -hen 8; Conserve
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US-11-096-568A-26217
US-11-096-568A-26217
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US-11-096-568A-26217
US-11-096-568A-26217
US-11-096-568A-26217
US-11-096-568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INV
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Publication No. US20060015951A1
GENERAL INFORMATION:
APPLICANT: Bulenberg, Karsten
APPLICANT: Moise, Martin
APPLICANT: Moiltor, Andreas
TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
FILE REFERENCE: 2923-696
CURRENT APPLICATION UNMERE: US/10/531,036
CURRENT APPLICATION UNMER: PCT/EP03/11352
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Pred. No. 33;
0; Mismatches 4; Indels
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i LOCATION: (1)..(558)
corner information: Ceres Seq. ID no. 13498878
US-11-096-5688-26217
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR PILING DATE: 2000-02-17
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR PILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALENTH Ver. 2.0
SEQ ID NO 16
LENGTH: 379
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Best Local Similarity 69.2%;
Matches 9; Conservative
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US-11-109-156-16
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Sequence 23045, Application US/11096568A

Publication No. US20060048240A1

ADMINISTRAL INFORMATION:
ADMINISTRAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUSZ
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

LENGTH: 249
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                                                                              Query Match 61.8%; Score 42; DB 7; Length 162; Best Local Similarity 66.7%; Pred. No. 30; Matches 8; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(249)
COTHER INFORMATION: Ceres Seq. ID no. 12411110
US-11-096-568A-23045
; LOCATION: (1)..(162)
; OTHER INFORMATION: Ceres Seq. ID no. 12635935
US-11-096-568A-641
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ORGANISM: Zea mays subsp. mays
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41 AARSGGGGGRP 52
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US-11-096-568A-23045
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March 13, 2006, 18:52:59; Search time 90.3529 Seconds (without alignments) $8.355 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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64
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003ss:* geneseqp2003bs:* geneseqp2004s:*

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
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	,		7 .	1	COOOL	
7	64	100.0	13	~	AAY06064	Aay06064 Human can
e	64	100.0	14	~	AAY05986	Aay05986 Human can
4	64	100.0	15	N	AAY05978	Aay05978 Human can
ഹ	64	100.0	20	~	AAY05979	Aay05979 Human can
9	64	100.0	30	Ŋ	AAU85105	
7	64	100.0	179	œ	ADK68648	Adk68648 Epitope l
œ	64	100.0	180	7	AAW62584	Aaw62584 Cancer as
6	64	100.0	180	7	AAW69665	Aaw69665 Human NY-
10	64	100.0	180	7	AAY05965	Aay05965 Human can
11	64	100.0	180	e	AAY52430	Aay52430 Human tum
12	64	100.0	180	m	AAY70862	Aay70862 Human tum
13	64	100.0	180	m	AAB03154	Aab03154 Human oes
14	64	100.0	180	4	AAB69946	Aab69946 Human NY-
15	64	100.0	180	4	AAG67164	Aag67164 Amino aci
16	64	100.0	180	4	AAU01535	Aau01535 Human NY-
17	64	100.0	180	4	AAE07714	Aae07714 Human NY
18	64	100.0	180	ß	AAU84818	Aau84818 Human NYN
19	64	100.0	180	Ŋ	AAU11543	Aaul1543 Human tum
20	64	100.0	180	9	ABR58672	Abr58672 Human can
21	64	100.0	180	9	ABR48210	Abr48210 Human bla
22	64	100.0	180	9	ABU56508	Abu56508 Lung canc
23	64	100.0	180	9	ABU56694	Abu56694 Lung canc
24	64	100.0	180	9	ABP74198	Abp74198 Human NY-

This peptide corresponds to amino acid residues 51-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HIA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

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64 100.0 180 6 ABR64816 Abr64816 Human NY- 64 100.0 180 6 ABR8438 AdC09576 Abr83438 Human NY- 64 100.0 180 7 AbD55564 Add35564 Human NY- 64 100.0 180 7 AbD55510 Add35568 Human NY- 64 100.0 180 7 AbD55510 Add35568 Human NY- 64 100.0 180 8 AbM72815 Adm73918 CACerfan 64 100.0 180 8 AbM72815 Adm73818 CACerfan 64 100.0 180 8 AbM73418 Adm73418 CAC-3 64 100.0 180 8 AbM73417 Adm318 CAC-3 64 100.0 180 8 AbM73417 Adm318 CAC-3 64 100.0 180 8 AbM73417 Add18451 Human NY- 64 100.0 180 8 AbM73418 Adm73418 CAC-3 64 100.0 180 8 AbM73415 Adm73418 CAC-3 64 100.0 180 8 AbM34153 Adm3418 CAC-3 64 100.0 180 9 AbM4353 Adm44353 Human aut 64 100.0 180 9 AbM4353 Adm44353 Human aut 64 100.0 180 9 AbM285096 Adv3880966 Tumor ant 64 100.0 180 9 AbM23374 Adm2828913 Add28913 Add289	100.0 180 9 AEA15651 Aea35651 100.0 240 9 AEB80047 Acb8047 100.0 240 9 AEB80047 Aeb80047 Aeb80047	06065 standard; peptide; 12 AA. 06065; NUG-1999 (first entry) an cancer antigen NY ESO-1/CAG-3 peptide.	NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; preast cancer; prostate cancer; proarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CTL.	18206-A2. PR-1999. EP-1998; 98WO-US01960 CT-1997; 97US-0061428 H ) US DEPT HEALTH & HU RF, ROSENDERG SA;	er antigen NY ESO1/CAG-3.
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 AAY06065 ID AAY06065 St XX AC AAY06065; XX		W09918206- 15-APR-199 21-SEP-199 08-OCT-199 (USSH ) US Wang RF,	Cancer

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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lymphoma; lolon cancer; metastasis; metanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; parcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                               Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
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                                                           AAY05986 standard; peptide; 14 AA.
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1997;
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                                                                                                                   16-AUG-1999
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                                                                                      AAY05986;
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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                    Gaps
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                                                                       Score 64; DB 2; Length 12;
Pred. No. 0.049;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                     Human cancer andigen NY ESO-1/CAG-3 peptide.
                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                 AAY06064 standard; peptide; 13 AA.
                                                                      Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer antigen NY ESO1/CAG-3.
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les 12; Conser
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                                            Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Matches
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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAYOS965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAYOS966), portions of them and their CC CAG-3 ORF1, CAG-3 ORF2 (see AAYOS966), portions of them and their CC CAG-3 ORF1, CAG-3 ORF2 (see AAYOS966), portions of them and their protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a CC transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 CC cancer peptide or tumour antigen; antibodies reacting with a CAG-3 CC for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is tranted by inducing cancer specific T cells in vitro for subsequent
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Claim 25; Page 50; 88pp; English.
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Matches 12; Conservative
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RESULT 4

2 ARASGPGGGAPR 13

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16-AUG-1999

AAY05978;

Homo sapiens.

WO9918206-A2

15-APR-1999

21-SEP-1998;

08-OCT-1997;

RF,

Wang

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uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                      NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
                                                                                                                                    metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
                                             Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US019609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0061428P.
      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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      16-AUG-1999
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                 WO9918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                            15-APR-1999.
                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU85105;
                                                                                                                                                                                                                        vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05955), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY0596-187), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or inhibiting cancer peptides; with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, tymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Malanoma is transfer by inducing cancer, specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukteemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; errical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine.
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                                                                                                                             Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 64; 88pp; English.
AAY05978 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US019609.
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                                                                                    (first entry)
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
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The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CMG-3 (or CMG-3) ORF1 (see AAY05965), and wand potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-CC 87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host calls (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antibodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, cuseful in diagnostic and detection assays; and methods for preventing or inhibiting cancer bedrides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cerrical cancers bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer specific T cells in vitro for subsequent return to a
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Query Match

Best Loca Matches

8 셤 AAY05979

RESULT 5 AAY05979 Epitope liberation-related NY-ESO-1 protein SeqID11.

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The invention rélates to a new synthetic polypeptide (1) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkede in the together in a different relationship relative to their linkage in the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polymeticotide encoding and a computer system for designing the synthetic polymetides. The synthetic polymetides and polymucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oesophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HVV (human immunistic virus, Epstein-Barr virus and respiratory and respiratory and respiratory and respiratory and respiratory and respiratory and membrate or infections caused by Neisseria, Meningococcal, Haemophilus, constitution or and and mycobacterium or paraaitic constitution and respiratory and mycobacterium or paraaitic constitutions and mycobacterium or and and mycobacterium or and and mycobacterium or and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
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        Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Glardia.
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                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                                                                                            25-MAY-2001; 2001WO-AU000622
                                                                                                                                                                                                                                                                                                                                                                                                                                   (AUSU ) UNIV AUSTRALIAN NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogen or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK36925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
                                                                                                                                                                                                                   WO200190197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomson SA,
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                                                                                                                                                            Homo
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This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope, wherein the substrate polypeptide sequence including the epitope, wherein the substrate polypeptide sequence including the epitope, wherein the substrate processing by a proteasome, contacting the substrate with a composition including the proteasome, and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasoide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention is useful for identifying a polypeptide suitable for epitope liberation, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitope. The compositions comprising the identified housekeeping epitopes. The compositions comprising the identified housekeeping proteason of expansion of cytotoxic T lymphocyte (CTL) to be used in adoptive immunotherapy. The invention is also useful cortivating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasone system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasone expressing target cells in the mathod of the pare in the composition as protein which is related to the contraction of a protein which is related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                   epitope liberation; substrate; proteasome; cytostatic; antibacterial; proteasoadide; fungloide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy, neoplastic cell; vitus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 11; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qiu Z,
                                                                                                                                                                                                                                                                                            07-NOV-2002; 2002US-00292413.
                                                                                                                                                                                                                                                                                                                                      07-NOV-2001; 2001US-0336968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simard JJL, Diamond DC,
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                                                                                                                                                                                                                                                                                                                                                                                               DIAMOND D C.
QIU Z.
LEI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-167209/16.
                                                                                                                                                                                                                                                                                                                                                                             (SIMA/) SIMARD J J
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wes 12; Conserv
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                                                                                                                                                                                                         US2003228634-A1.
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                 11-DEC-2003.
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(QIUZ/)
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ID AAW6
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Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

formerly known as LL-1.2 clone.

Human NY-ESO-1 protein sequence,

(first entry)

27-0CT-1998

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of onset of a cancerous condition, comprising monitoring a sample from a parameter selected from NP-ESO 1 protein, a peptide derived from NY-ESO-1 protein, and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression
                                                                                                                                                                               Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential myristorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                         Cancer associated antigen NY-ESO-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scanlan M, Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US016335
                                                            (first entry)
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N-PSDB; AAV38566.
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                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drijfhout JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1997;
                                                            17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9814464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1998
AAW62584;
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New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.

Example 2; Page 57-58; 73pp; English.

Boon-Falleur

Godelaine D,

Smet C,

WPI; 1998-427951/36. Lethe B, Lucas S,

N-PSDB; AAV50348

(LUDW-) LUDWIG INST CANCER RES

98WO-US001445. 97US-00791495.

27-JAN-1998; 27-JAN-1997;

30-JUL-1998.

WO9832855-A1 Homo sapiens

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The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGB-1 tumour associated protein (TAP). The present invention also describes LAGB-1 tumour associated protein (TAP). The present invention class describes (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder expression product, comprising administering a LAGE-1 TAP or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for electively enriching a population of T cells with cytolytic T cells of the comprising contexting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an elective the comprising accepted to the complex of a LAGE TAP or an elective the comprising accepted to the cytolytic T cells or a LAGE-1 TAP comprising accepted to the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the complex of a LAGE TAP or an elective the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Gaps ö

100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.51; ive 0; Mismatches 0; Indels

0;

llarity 100.0%; Conservative

Query Match Best Local Similarity

12;

Best Loca Matches

1 ARASGPGGGAPR ARASGPGGGAPR

ò 유 AAW69665 standard; protein; 180 AA.

AAW69665 ID AAW6 RESULT 9

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hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma
                        Homo sapiens.
Unidentified.
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   The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content the tunour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides and their variants (see AAY05965-CAAY05966), portions of these peptides that includes recipient from development of cancer. The invention provides: vectors and host cells car transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of the cancer peptide, useful in diagnostic and detection assays; and methods content perputation of the cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, broatian, pancreatic and adenocarcinomas such cancer peptide by inducing cancer, specific T cells in vitro for subsequent
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           non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastassis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; ORFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell; cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
   ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 2; Length 180;
Pred. No. 0.51;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                         Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                          98WO-US019609
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(first entry)
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                                                                                                                                                                                                                                Rosenberg SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          return to a patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA;
                                                                                     Homo sapiens.
                                                                                                         WO9918206-A2.
                                                                                                                                                                                08-OCT-1997;
                                                                                                                                                          21-SEP-1998;
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15-FEB-2000
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Class I HLA-A24 and HLA-
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                                                                                                                                                                                                 'note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                    .92
:e= "Peptide presented by MHC Class I HLA-B7, HLA-B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Peptide presented by MHC Class I HLA-B7 and
                                                                                                                                                                                                                                                                                                                   "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Peptide presented by MHC Class I HLA-B44"
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                                                                                                                                                                                                                                                                     .90
te= "Peptide presented by MHC Class I HLA-Al"
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ils. .124
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note= "Peptide presented by MHC Class I HLA-B7"
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                                                              presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                      "Peptide presented by MHC Class I HLA-Al"
                                  "Peptide presented by MHC Class I HLA-B7"
                                                                                                   HLA-B7"
                                                                                                                                                                    "Peptide presented by MHC Class I HLA-B7"
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e= "Peptide presented by MHC Class I
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/note= "F
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Klade C;

Peptide Peptide 28-OCT-1999

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The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF). I that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the CAMEL (Cytotoxic T lymphocytes (CTL) recognised Antigen on MELanoma) protein, a tumour-asociated antigen. The tumour-associated antigen displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma; melanoma; ovary; testis; transmembrane domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 3; Length 180; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Potential N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Potential N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM INT GMBH. (UYHO-) UNIV HOSPITAL LEIDEN.
                                                                                                                                                                                                                                                                                                                Schrier PI, Aarnoudse CA, Heider K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 62-63; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB03154 standard; protein; 180 AA.
                                                                                                                                               99WO-EP007832
                                                                                                                                                                                            98EP-00119583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-339685/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD00152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion proteins
                                                    WO200023584-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
       Homo sapiens
                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                            16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB03154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA library. Tissue, localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, trumour cell lines with some degree of frequency - these included melanoma specimens and cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY - ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class I HIA-A2 molecules, thereby stimulating and class II Molecules for presentation to T-cells. Peptides AAV52431-C Y52444 bind to Class I HIA-A2 molecules, thereby stimulating to Class II HIA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and cancer such as melanoma. Dreast cancer lung research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NY-ESO-1; CAMEL, CTL-recognised Antigen on MELanoma; human, cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                 Chen Y, Scanlan M, Alexander K, Old LJ;
                                                                  /note= "Peptide presented by MHC Class I HLA-B52"
159. .167
'note= "Peptide presented by MHC Class I HLA-A3"
62. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 3; Length 180; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour antigen, NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian cancer, thyroid cancer, bladder
stimulate the proliferation of T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY70862 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 30; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                            98US-00062422.
98US-00165546.
                                                                                                                                                                                                                99WO-US006875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                 Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-038483/03.
N-PSDB; AAZ38380.
                                                                                                                                                                                                                                                                                                                                                                            Stockert E, Jager
Gure A, Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 AA;
                                                                                                                 WO9953938-A1
                                                                                                                                                                                                                                                               17-APR-1998;
                                                                                                                                                                                                                                                                                   02-OCT-1998;
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AAY70862;

Query Match

Best Loca Matches

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Gaps

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0; Indels

Chen Y, Scanlan M;

Knuth A,

old LJ,

2001-182822/18.

CANCER RES

99US-00359503

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Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a
                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                      (SLOK ) SLOAN KETTERING INST C (CORR ) CORNELL RES FOUND INC.
                                                                                  14-JUL-2000; 2000WO-US019220.
                                                                                                                                                                                                Jager E, Stockert E,
                                                                                                                                                                                                                            WPI; 2001-182822/
N-PSDB; AAF58634.
                            WO200107917-A1
 Homo sapiens.
                                                                                                              23-JUL-1999;
                                                        01-FEB-2001
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA encoding this sequence was isolated from a CDNA call this sequence was isolated from a CDNA cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell innew and in normal overy and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristcylation sites and 0-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The artigen is useful as an immunogen when combined with an adjuvant, in both precursor and post-translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a marker for the targetted delivery of therapeutic agents to besophageal cancer cells. It targetted delivery of therapeutic agents to besophageal cancer cells. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                      New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions. e.g. infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                    Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can also be used to generate diagnostic or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 3; Length 180;
Pred. No. 0.51;
0; Mismatches 0; Indels
       /note= "Potential O-phosphorylation site"
138
                                         /note= "Potential O-phosphorylation site"
                                                      152. .172
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                    Scanlan M, Gure AO, Chen Y, Tureci O, Old LJ;
                                                                                                                                                                                                            KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69946 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 3; 9pp; English.
                                                                                                                                                                                                            (SLOK ) SLOAN KETTERING INST CF
(CORR ) CORNELL RES FOUND INC.
(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                                                                                      98US-00013150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ARASGPGGGAPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NY-ESO-1 protein.
                                                                                                                                                                                                                                                                                                             WPI; 2000-410880/35.
N-PSDB; AAA61483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180 AA;
Modified-site
                          Modified-site
                                                                                                                                                      26-JAN-1998;
                                                                                                                                                                                  03-OCT-1996;
                                                                                              US6069233-A
                                                                                                                          30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69946;
                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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                                                     The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a amererous acondition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value botained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 64; DB 4; Length 180; 100.0%; Pred. No. 0.51; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG67164 standard; protein; 180 AA.
Example 5; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2001; 2001WO-US002126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2000; 2000US-00510635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200162917-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG67164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The present sequence represents cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (HRC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of cancer, especially testis tumours
                                                                                                                                                  Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumors.
                                                                                                                                                                                                         Example 5; Fig 3; 50pp; English.
                 (LUDW-) LUDWIG INST CANCER RES.
                                                       Lethe B, Boon-Falleur T;
                                                                                          WPI; 2001-550091/61.
N-PSDB; AAH75118.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 180 AA;
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Gaps ; 0 Query Match 100.0%; Score 64; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.51; Matches 12; Conservative 0; Mismatches 0; Indels 1 ARASGPGGGAPR 12 ઠે

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Search completed: March 13, 2006, 19:03:59 Job time: 90.3529 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24 ; Search time 14.258B Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-29 64 Perfect score:

1 ARASGPGGGAPR 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq lengt; 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR 80:* Database

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description
1	44	68.8	3190	. ~	T13828	CREB-binding prote
8	42	9.59	185	7	T36874	prot
m	42	9.59	201	7	G72663	hypothetical prote
4	42	9.59	222	~	T36115	σ
Ŋ	42	9.59	327	~	T29031	hypothetical prote
9	42	65.6	351	~	S50754	
7	42	9.59	378	~	C87425	-
80	42	65.6	436	N	T36104	conserved hypothet
σ	42	9.59	474	~	G75580	conserved hypothet
10	41	64.1	173	~	AB3648	flagellar basal-bo
11	41	64.1	286	~	S04673	H+-transporting tw
12	41	64.1	357	7	F82878	XAA-PRO aminopepti
13	41	64.1	371	7	T39312	hypothetical prote
14	41	64.1	505	~	S68518	tub protein, brain
15	41	64.1	521	~	A29345	steroid hormone re
16	41	64.1	1207	N	T00378	KIAA0641 protein -
17	41	64 .ਜੂ	1690	~	T35694	ATP dependent DNA
18	40	62.5	82	7	T04476	acclimation protei
19	40	62.5	290	~	T36712	hypothetical prote
20	40	62.5	335	~	S08341	
21	40	62.5	379	7	A48082	
22	40	62.5	383	~	A86182	hypothetical prote
23	40	ö	619	~	802165	-
24	40	62.5	910	~	A34721	androgen receptor
25	40	ς.	911	~	B34721	androgen receptor
56	40	'n	919	~	A39248	
27	4	62.5	954	7	A87431	regulatory protein
28	39.5	61.7	730	~	A36226	collagen alpha 1 c
29	39	6.09	103	~	C72683	hypothetical prote

Pur beta - human (	competence/damage-	histocompatibility	hypothetical prote	polygalacturonase	DNA-invertase - Rh	probable transcrip	transcription acti	polygalacturonase	hypothetical prote	hypothetical prote	Ca2+/calmodulin-de	Ca2+/calmodulin-de	endopeptidase Clp	polygalacturonase	polygalacturonase
B45036	E87464	900691	T35619	S25825	S42585	F95899	A47008	S25824	B72677	S55626	S28184	JC1451	T52451	830067	830066
~	N	7	~	7	~	~	~	~	~	~	~	7	~	~	0
114	163	166	187	197	213	260	569	306	307	349	377	380	387	410	410
	_	•	σ.	σ	6	σ	σ	σ	σ	σ.	σ	9	σ	6	σ
6.09	60.9	90	9	.09	60.	60.	60.	90.	60.	60.	.09	.09	60.	90	60.9
			0	39 60.	σ	6			9	9	σ		6	0	6

## ALIGNMENTS

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CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Accession: T13828
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G. Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Accession: T13828
A;Accession: T13828
A;Accession: UNIPROT: O01368; UNIPARC: UPI000003EB83; EMBL: U88570; NID:g1916929; P:C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>
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320 NGPGGGGPR 328 4 SGPGGGAPR 12 g ઠે

RESULT T36874

hypothetical protein SCI51.11c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T36874

R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
A;Reference number: Z21617
A;Accession: T36874
A;Accession: T36874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A)Residues: 1-185 <MUR>
A)Cross-references: UNIPROT: Q9S229; UNIPARC: UPI0000DB31A; EMBL: AL109848; PIDN: CAB52835
A)Experimental source: strain A3(2)
C)Genetics:

A; Gene: SCOEDB: SCI51.11c

Gaps ö Query Match 65.6%; Score 42; DB 2; Length 185; Best Local Similarity 80.0%; Pred. No. 50; Matches 8; Conservative 0; Mismatches 2; Indels 2; Indels

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1 ARASGPGGGA 10

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Gaps

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-327 «MUX-
A;Kesidues: 1-327 «MUX-
A;Cross-references: UNIPROT:001799; UNIPARC:UPI0000078FFF; EMBL:AF003139; PIDN:AAB54156.
A;Experimental source: strain Bristol N2; clone F53G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: $50754
R;Woessner, U.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring, Blant Mol. Biol. 26, 947-960, 198 as a several volvocalean cell wall proteins.
A;Reference number: $50754; MUID:95093034; PMID:8000007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 «STD>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q39492; UNIPARC:UP100000A170A; EMBL:L29028; NID:g530877; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                          Length 327;
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    Caulobacter crescentus

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81;
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86;
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Pred. No. 91;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein WP6 - Chlamydomonas eugametos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
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77.88;
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80.0%;
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C,Superfamily: aldose 1-epimerase
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Best Local Similarity Burgerive
Best Local Similarity
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                   A;Gene: CEGP: F53G12.7
A;Map position: 1
A;Introns: 59/3; 138/1; 223/2
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282 NGPSGGAPR 290
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A Molecule type: mRNA
A Residues: 1-351 <WOE>
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                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72663
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jan-no, K.; Takah A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUD:99310339; PMID:10382966
A;Stetus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-201 «KAW»
A;Cross-references: UNIPROT:09YE35; UNIPARC:UPI000005DC7C; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
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A;Experimental source: strain A3(2)
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A;Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMEÇ Data Library, April 1999
A;Reference number: 221597
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R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A;Peference number: Z20555
A;Reference number: Z20555
A;Accession: T29031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T36115
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0734
                                                                                                                                                                         hypothetical protein APE0734 - Aeropyrum pernix (strain Kl)
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
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Best Local Similarity 75.0
Matches 9; Conservative
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86 ARGSGPGSGA 95
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Gaps ö

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A;Molecule type: DNA
A;Residues: 1-173 «KUR»
A;Residues: 1-173 «KUR»
A;Residues: 1-173 «KUR»
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UP10000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
A;Experimental source: strain 16M
A;Gene: BMSI11107
A;MAP position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H+-transporting two-sector ATPase (BC 3.6.3.14) gamma chain - Rhodopseudomonas blastica C,5pecies: Rhodopseudomonas blastica C;5pecies: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004 C;Accession: 804673
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-357 <CLA>
A,CLAS
A,CCOSS-references: UNIPARC:UPI0000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
A,Experimental source: serovar 3; blovar 1
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A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ritybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
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C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C,Accession: F82878
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A; Residues: 1-286 <TYB>
A; Cross-references: UNIPROT: PD5436; UNIPARC: UPI0000126582
C; Superfamily: H(+)-transporting ATP synthase gamma chain
C; Keywords: ATP biosynthesis; hydrolase; membrane-associated complex
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                                                                                                                                                                                                                                                                                                            Length 173;
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                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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66;
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Pred. No. 99;
0; Mismatches
                                                                                                                                                                                                                                                                                                    64.1%; Score 41; DB 100.0%; Pred. No. 66; ive 0; Mismatches
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A,Genetic code: SGC3
C,Superfamily: X-Pro aminopeptidase
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80.0%;
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Best Local Similarity 80.0.
Local 8; Conservative
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Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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S04673
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R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Vamathevan, J.J.; Fraser, C.M.
Science 286, 1571-1577, 1999;
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MuID:20036896; PMID:10567266
A.Accession: G75580
A.Accession: G75580
A.Accession: G75580
A.Residues: 1-474 <MID.
A.Residues:
                                                                                              Conserved hypothetical protein SCEIS.01 - Streptomyces coelicolor (fragment)
C; Species: Streptomyces coelicolor
C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C; Accession: T36104
R; Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B; Murphy, L.; Harris, Data Library, April 1999
A; Reference number: Z21597
A; Reference number: Z21597
A; Reference preliminary; translated from GB/EMBL/DDBJ
A; Residues: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-436 eMUR>
A; Residues: L436 eMUR>
A; Residues: L436 eMUR>
A; Residues: L436 eMUR>
A; Reperimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SCEIS.01
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selvov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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C,Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821
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Pred. No. 1e+02;
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Best Local Similarity 72.7%;
Matches 8; Conservative (
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nes 8; Conservative
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Matches
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Gaps

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A; Residues: 1-521 «GIO»

A; Residues: 1-521 «GIO»

A; Cross-references: UNIPROT:P11474; UNIPARC:UDIO00142399; EMBL:X51416; NID:g36608; PIDR.

B; Wiley, S. R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.

Genes Dev. 7, 2206-2219, 1993

A; Title: SV40 early-to-late switch involves titration of cellular transcriptional representations and the procession: A49074

A; Reference number: A49074

A; Reference trupe: protein

A; Rolecule type: protein

A; Ross - references: UNIPARC:UPI00017A1DF

C; Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi' F; 174-434 Domain: erbA transforming protein homology «ERBA»

F; 176-196/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.1%; Score 41; DB 2; Length 521; 66.7%; Pred. No. 1.6e+02; ive 1; Mismatches 3; Indels
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Job time : 14.2588 secs
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462 AGRAGPGGGAER 473
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Matches 8; Conserv
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C. Species: Mus musculus (house mouse)
C. Accession: S6818; S68519
R. Noben-Trauth, K.; Naggert, J.K.; North, M.A.; Nishina, P.M.
R. Noben-Trauth, K.; Naggert, J.K.; North, M.A.; Nishina, P.M.
Nature 380, 534-538, 1996
A. Title: A candidate gene for the mouse mutation tubby.
A. Reference number: S68518; MUID:96195061; PMID:8606774
A. Accession: S68518
A. Status: preliminary; nucleic acid sequence not shown
A. Molecule type: mRNA
A. Residues: 1-505
A. Accession: S68519
A. Accession: S68519
A. Accession: S68519
A. Accession: S68519
A. Residues: 47-505
A. Residues: Lobby
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Bubmitted the EMBL Data Library, March 1998
A;Reference number: Z21843
A;Accession: T39312
A;Accession: T39312
A;Accession: T39312
A;Reticus preliminary, translated from GB/EMBL/DDBJ
A;Residues: 1-371 < WOO>
A;Residues: 1-371 <
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                                                                                                                                                           Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                              protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
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A;Map position: 2
A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914; Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S., Williamson B., Stockert E., Pfreundschuh M., Old L.J.; Hantigen aberrantly expressed in human cancers detected by autologous antibody screening.";
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10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
HMD1, AJ275978; CAB76945.1; -; mRNA.
HYDOChetical protein.
NON TER
SEQÜENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
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Q8NZ61 9DBLT
Q94LD1_ORYSA
Q4NZ7 9DBLT
Q7QEK5_ANOGA
Q4SW43 TETNG
Q4NWX4 9DBLT
G5NTAS_CANFA
G63NC9 BURPS
Q63NC9 BURPS
Q62DA7_BURMA
Q63NC9 BURPS
Q67UNB_ORYSA
G67UNB_ORYSA
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Q9NY13;
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   Nelson D.L.;
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Matches
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   RA REPRESENTATION OF SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Galgoczy P., Rosenthal A., Platzer M.;
"Human-mouse comparative sequence analysis of the NEMO gene reveals an alternative promoter within the neighboring G6PD gene.";
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                 Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen B., Boon T., H., T., a new gene with tumor specificity."; Int. J. Cancer 76:303-908(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                     WEDLINE=98430682; PubMed=9759882; Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.; Schwartzentruber D.J., Rosenberg S.A.; The send melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames."; J. Immunol. 161:3596-3606(1998).
-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in utcrine myometrium.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 1; Length 180;
Pred. No. 0.17;
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Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
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Gly-rich.
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U87459; AAB49693.1; -; mRNA.
EMBL; AJ003149; CAR05508.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
HGNC; HGNC; 2491; CTAGIB.
                                                                                                                    MEDLINE=98289662; PubMed=9626360;
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
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Q7LBY4 HUMAN
ID Q7LBY4_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    igen; Transmembrane.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDIJNE=99454989; PubMed=10523621;

DE Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;

Do Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;

"DNA methylation is the primary silencing mechanism for a set of germ "DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";

Mol. Cell. Biol. 19:7327-7335(1999).
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Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
de Plaen E., Boon T.;
"LAGE-1, a new gene with tumor specificity.";
Int. J. Cancer 76:903-908(1998).
"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
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CTAG2 HUMAN STANDARD; Q9UJ89; Q9Y479;
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
Name=CTAG2; Synonyms=ESO2, LAGE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lethe B.G.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                            Platzer M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galgoczy P., Platzer M.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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Akking T., Croseman L.C., Pitt T., Churcher C., Mungall K.L.,
Bentley S.D., Sebainia M., Thomson N.R., Bason N., Beacham I.R.,
Bentley S.D., Sebainia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,
Pelthwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Songaivilai S., Stevens K., Tumapa S., Vesaratchavet M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
NCBI_TaxID=28450;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
EMBL, BX571965; CAN36946.
GO; GO:0003897; F.DNA-directed DNA polymerase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR010372; DNA pol3 delta.
InterPro; IPR010373; DNA pol3 delta.
Pfam; PF06144; DNA pol3 delta; I.
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Pred. No. 9.3;
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Last annotation update)
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerase III, delta subunit (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K96243;
PubMed=15377794; DOI=10.1073/pnas.0403302101;
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                                                                                                                                                                                                                                                                                                     Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
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Q62H22;
                                                                                                                                                                                         BURPS PRELIMINARY;
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                                                                          51 ARASGPRGGAPR 62
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es 10; Conservative
                                 1 ARASGPGGGAPR 12
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обзотв;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
Raha S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
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use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQRPGTPGPPPEGAQGOGCRGVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poły-Pro.
MSVWDQDREGAGRMRVVGWGLGSASPEGOKARDLRTPKHKV
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Went=Alternative splicing; Named isoforms=2;
Name=LAGB-1B; Synonyms=LAGB-1L;
IsoId=075638-1; Sequence=Displayed;
Name=LAGB-1A; Synonyms=LAGB-1S;
IsoId=075638-2; Sequence=VSP_004301;
TISSUB SPRCIFICITY: Testis and very low level in placenta and in melanomas, non-small-cell lung carcinomas, bladder, prostate and head and neck cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: A transmembrane domain is present in isoform LAGE-1A. SIMILARITY: Belongs to the CTAG family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing; Antigen; Polymorphism; Transmembrane.
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Pred. No. 2.8;
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8BE0EE00AE55E8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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FTId=VAR_007856.
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EMBL, AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL, AJ223040; CAA11043.1; -; mRNA.
EMBL, AJ223041; CAA11044.1; -; mRNA.
EMBL, AJ012834; CAA10194.1; -; mRNA.
EMBL, AJ012835; CAA10196.1; -; mRNA.
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Ensembl; ENSG0000126890; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA; 21120 MW;
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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A Straubberg R.L., Feingold E.A., Grouse L.H., Darged J.G.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhart N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhart N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Erownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

B Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Radan A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Nhiting M., Madan A., Young A.C., Schwuckenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerction and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Peldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.P.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Erroc. Natl. Acad. Sci. Uls. A. 101:14246-14251 (2004).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                 GO, GO:0003887, F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016560; P:DNA replication; IEA.
InterPro; IFR010372; DNA pol3 delta.
InterPro; IFR005790; DNA pol3 delta.
Pfam; PF06144; DNA pol3 delta; 1.
TIGREAMS; TIGR01128; holA; 1.
TIGREAMS; TIGR01128; holA; 1.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                      Score 54; DB 2; Length 362; Pred. No. 9.3;
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Director MGC Palject;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015174; AAH15174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AA
                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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1 Similarity 83.3%;
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96BU2 HUMAN PRELIMINARY;
Q96BU2;
                                                                                                                                                                                                                                                                                                                                                                                  348 ARAAGPGGDAPR 359
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                      TIGR; BMA2451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PLEKHG2;
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Q96BU2 HU
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MEDINES DENGEMBER 12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINES R.D., Colling F.S., Magner L., Schaefer C.F., Bhat N.K., A tischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A dichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Braha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., A Hakealey R.W., Touchman J.W., Garen B.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                               Gaps
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                                                                           Length 194;
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                                                                                                                            2; Indels
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Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC013426; AAH13426.1; -; mRNA.
SEQUENCE 896 AA, 94247 MW; 0DE6869BCFD4C471 CRC64;
1
194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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(TrEMBLrel. 28, Last sequence update)
                                                                         DB 2;
19;
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                                                                                                                                                                                                                                                                                                                                                                  896 AA.
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Pred. No. 84;
0; Mismatches
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                                                                           78.1%; Score 50;
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81.8%;
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                                                                                                    81.8%;
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ID GEDHVE HUMAN PRELIMINARY;
AC GEDHVE;
DT 25-0CT-2004 (TrEMBLrel. 28
DT 25-0CT-2004 (TrEMBLrel. 28
                                                                                                                                                                                                                                                                                                                                                             Q96D18_HUMAN PRELIMINARY;
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                               9; Conservative
                                                                                                                                                                                                                                   99 ARROGPGGGAP 109
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Name=PLEKHG2;
Homo sapiens (Human).
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                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE
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Matches
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RAY PURDEGLIANOZOSAY, DOI-10.11038/NG1248,

RAY PURDEGLIANOZOSAY, DOI-10.11038/NG1248,

RAY RAKAMATSUN A., NISHIKAWA T., OTSUKIT, NISHIZARA T., TITIE R.,

RAY SAKINE M., OBAYASHI M., NISHI T., Shibahara T., Tanaka M., Takahashi M., Yanda T., Takaha T., Tanaka M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., RA Sugawara M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., RA Tanikawa M., Momiya K., Takahashi T., Yamashita H., Murakawa K., RA Ishida S., Ono Y., Takayachi-Fujii A., Hara H., Tanase T.-O., RA Ishida S., Ono Y., Takayachi-Fujii A., Hara H., Tanase T.-O., RA Imose N., Masunawa H., Ichihara R., Takeuchi K., Aita M., Acteuka S., Momiyama H., Sacoh N., Takami S., Tersahima Y., Saroh S., Momiyama H., Sacoh N., Takami S., Tersahima Y., Sano S., Amazaki M., Watanabe T., Sujiwama T., Shiohata N., Kawakami B., Yamazaki M., Watanabe T., Sujiwama T., Shiohata N., Kawakami Y., Rawabata A., Hikiji T., Kobatake N., Takemoto M., Chimori Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Rayabata A., Hikiji T., Kobatake N., Takahashi Y., Nakagawa K., Sanba T., Matsumura K., Nakagawa M., Sasaki M., Takahima Y., Matsumura K., Nakagawa M., Sasaki M., Watahima M., Hata H., Watanabe M., Komatsu T., Sugano S., Matsumura K., Nakagima Y., Matanabe M., Komatsu T., Sakaki M., Matania Y., Matania Y., Matanabe M., Komatsu T., Sugano S., Matsumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Rompila R., Nakamura Y., Ohara O., Isogai T., Sagan J., Sagan J., Sagan J., Nompila R., Nompila R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sagani J., Nakamura Y., Ohara O., I
                                                             TISSUE-Spleen;
PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00233; PH; 1.
SMART; SM00325; RhoGBF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001849; PH. InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSZ8E2_ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335 ARROGPGGGAP 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 81.8
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARASGPGGGAP 11
        [1]
NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNAB. ";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORYSA
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0528E2 ORY
0528E2 ORY
0528E
AC 0528E
DT 25-0C
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DT 25-0C
DT 25-0C
OR Name=
OS Oryza
OC BUKAR
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                                                                                                                                                                                                                                                                                                                 Straubberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carannoi P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Whiting M., Madan A., Young A. Schwichenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Generation and initial analysis of more than 15,000 full-length human
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                         PLEKHG2 protein (Fragment).
Name=PLEKHG2;
Name=PLEKHG2;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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0
                                                                                                                                                                                                                                                                    TISSUE-Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.1%; Score 50; DB 2; Length 1253; 81.8%; Pred. No. 1.2e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Contains 1 PH domain.
EMBL; BC07588; AAH75688.1; -; mkNA.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
Pfam; PF00621; RhoGEF; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FLJ00018 protein (Fragment)
Name-PELEKHGZ; Synonyms=FLJ00018;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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SMART; SM00325; RhoGEF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 81.8
les 9; Conservative
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                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                     NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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Q9H7P9 HUMAN
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Matches
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Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.1%; Score 50; DB 2; Length 1430; 81.8%; Pred. No. 1.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1430 AA; 152528 MW; E4DF0BFDACCB6A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q528E2,
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein P0487E11.17.
                                                                                   Ensembl, ENSG0000090924; Homo sapiens.
HGNC; HGNC: 29515; PLEKHG2.
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AK024429; BAB15719.1; -; mRNA.
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Hypothetical protein OJ1191_A10.131 (Hypothetical protein OJ1014_E06.5).
Name=OJ1191_A10.131; Synonyms=OJ1014_E06.5;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                  Gramene, QFFIE3; -. Gubiquitin ligase complex; IEA. GO; GO:0000151; C:ubiquitin ligase complex; IEA. GO; GO:0046872; F:metal lon binding; IEA. GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA. GO; GO:0008270; F:zinc ion binding; IEA. GO; GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                   Sasaki T., Mateumoto T., Yamamoto K.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.-I- SUMLIARITY: Contains I RING-type zinc finger. EMBL; AP0038857; BAD08744.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 449 AA, 47196 MW; BBEFF7708B292296 CRC64;
                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 29, Last annotation update)
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7
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InterPro; IPR001841; Znf_ring.
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Local Similarity 75.0%;
les 9; Conservative
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SRAKGGGGGAPR 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARASGPGGGAPR 12
                05-JUL-2004 (TrEMBLrel
05-JUL-2004 (TrEMBLrel
01-FEB-2005 (TrEMBLrel
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                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                            NCBI_TaxID=39947;
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                                                                  Assaki T., Matsumoto T., Yanamoto K., Sakata K., Baba T., Katayose Y., A., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokwa S., Masukwa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijina M., Ikeda M., Ikeno M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi M., Koni Y., Nachita K., Machara T., Mizuno H., Mizubayashi T., Naka Y., Nakamira M., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Nakamiki N., Nagishim., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K., Maniki N., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Yano M., Jiang J., Gojobori T., Ruture 420:312-316(2002).

R EMBL, Apologyay: Babbayaze.i, -; Genomic_DNA.
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";

Hum. Mol. Genet. 10:339-352(2001).

EMBL, AE006463; AAK61225.1; -; Genomic_DNA.

Ensembl; ENSCO000167933; Homo sapiens.

Hypothetical protein.

SEQUENCE 321 AA; 32979 MW; 9C8764CFA17P4CPA CPCAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                      MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 48; DB 2; Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 262 AA; 27141 MW; 816A1189E43BA42A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gene X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AA.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 83.3%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96S27 HUMAN PRELIMINARY;
Q96S27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7F1E3_ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 ARASGDGGGADR 236
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Best Local Similarity
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Q7F1E3 ORYSA
ID Q7F1E3 OF
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RESULT 12
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
;
2; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0063J18.9.
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STRAIN=2CP-C;
STRAIN=2CP-C;
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome assembly of Anaeromyxobacter 'sadenalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=2CP-C;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
Larimer F., Land M.;
Larimer F., Land M.;
Larimer F., Land M.;
Larimer C., Land M.;
Annotation of He draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-: CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.

EMBL, AAHD01000013; EAL79351.1; -; Genomic_DNA.

SEQUENCE 895 AA; 93871 WW; 0AE25BBBF17ZBDB0 CRC64;
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Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
                                                                                                                                                                                    Query Match 73.4%; Score 47; DB 2; Length 367; Best Local Similarity 75.0%; Pred. No. 96; Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.4%; Score 47; DB 2; Length 895; Best Local Similarity 81.8%; Pred. No. 2.38+02; Matches 9; Conservative 0; Mismatches 2; Indels
Gramene; Q6AV33; -.
Hypothetical protein.
SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         895 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Q4NUK4;
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ORFNames=AdehDRAFT_2813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
O4NUK4 9DELT
O4NUK4 9DELT
D1 3-SEP-20
DT 13-SEP-20
DT 13-SEP-20
DT 13-SEP-20
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CO CYSTODACO
OC BACTERIA
CO BATTERIA
RY NUCLEOTII
RY COPELADA
RY GENALOS
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Search completed: March 13, 2006, 19:14:28 Job time: 88.1059 secs

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Sequence 29111, A Sequence 17831, A Sequence 2. Appli Sequence 25. Appli Sequence 21, Appl Sequence 1872, A Sequence 29442, A Sequence 19986, A Sequence 562, Appl Sequence 6, Appli Sequence 2, Appli

OM protein

Run on:

Sequence:

Searched:

Database

Result No.

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100.0%; Score 64; DB 1; Length 180; 100.0%; Pred. No. 0.21; rive 0; Mismatches 0; Indels
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 40,212
REFERENCE/DOCKET NUMBER: 10461/7005
TELEPRONE: 617-720-2441
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
CRANGING CHARACTERISTICS:
CRANGING CHARACTERISTICS:
CHARACTERISTICS:
US-09-252-991A-17764
US-09-252-991A-17811
US-08-252-991A-7831
US-08-660-765A-2
US-09-252-991A-25611
US-09-491-356C-21
US-09-252-991A-31279
US-09-252-991A-31279
US-09-252-991A-31279
US-09-252-991A-30723
US-09-252-991A-19966
US-09-949-002-562
US-08-949-002-562
US-08-949-016-7812
US-08-949-016-7812
US-08-630-522
US-08-630-522
US-08-630-522
US-08-630-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STREFF:
                                                                                                                                                                                                                                                                                                                                                        US-09-032-365A-2
                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 180 amino acids
amino acid
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Matches 12; Conservative
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    TOPOLOGY: linear
MOLECULE TYPE: protein
    JS-08-791-495-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-791-495-9
    Query Match
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Sequence 8, Appli
Sequence 25, Appli
Sequence 15, Appli
Sequence 30, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 117, Appli
Sequence 1749, Appli
Sequence 1749, Appli
Sequence 1749, Appli
Sequence 1749, Appli
Sequence 3, Appli
Sequence 24923, Appli
Sequence 23226, Appli
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Sequence 20577, A
Sequence 30527, A
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Sequence 27111,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       March 13, 2006, 19:14:49; Search time 22.3059 Seconds (without alignments) 44.477 Million cell updates/sec
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                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgr2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgr2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgr2_6/ptodata/1/iaa/RB_COMB.pep:*
6: /cgr2_6/ptodata/1/iaa/RB_COMB.pep:*
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US-08-937-265B-8
US-09-391-7265B-8
US-09-392-714-25
US-09-341-828A-9
US-09-341-828A-9
US-09-341-828A-9
US-09-341-828A-7
US-09-32-991A-717349
US-09-252-991A-3295
US-09-252-991A-3295
US-09-252-991A-3295
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US-09-902-540-11047
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                           US-09-529-206E-29
64
                                                                                                                                                                                                                                                                  1 ARASGPGGGAPR 12
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100
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Gaps

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COUNTRY:
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                                                                              Sequence 8, Application US/08937263B

Patent No. 6274445

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
TITLE OF INVENTION: INSOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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APPLICANT: Stockert, Elisabeth; Jager, Elke;

APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;

APPLICANT: Knuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer

TITLE OF INVENTION: Associated Proteins, Uses Thereof,

TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA

TITLE OF INVENTION: Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 64; DB 2; Length 180; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CODNIKA,
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
CAMPITER: IBM
CAMPITER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Pulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fulbright & Jaworski, L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
FRIOR APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
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; TOPOLOGY: linear
US-08-937-263B-8
                                                                           US-08-937-263B-8
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Gaps
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100.0%; Pred. No. 0.21;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.21;
tive 0; Mismatches 0; Indels
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US-09-392-714-25

US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 668647

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Garalan, Ali O.
APPLICANT: Grant Ali O.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: UNMBER: US/09/392,714A

CURRENT FILING DATE: 1999-09-09

EARLIER FILING DATE: 1998-09-09

SARLIER FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0

TYPER: PRT

COCANATOR TOTAL
COUNTY. 10103
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
AMDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                      PRIOR ADDITION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION NUMBER: 09/725,182
FILING DATE:
PRIOR APPLICATION NUMBER: 08/725,182
FILING DATE: 0ccober 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPRAX: (212) 752-5598
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
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Best Local Similarity 100.
Matches 12; Conservative
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US-09-392-714-25
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TOPOLOGY: linear
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    <151> 1998-01-27
                                                                                                                                                                                                    100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.21;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Yao-Tseng
ITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (ARV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER: PS ED IN NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCE 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                 Mismatches
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PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
NUMBER: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
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Patent No. 5811519
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600 Atlantic Avenue
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                          1 ARASGPGGGAPR 12
                                                                                                                                                                                                                                                                                                                                    51 ARASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                       Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                        US-09-341-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-849-602-30
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LENGTH: 180
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                                                                                                                                                                                                    Query Match
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                                                                                                     APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 64; DB 2; Length 180; 100.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09341829A
Patent No. 6794331
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: L0461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495 <151> 1997-01-2
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: 1BM
OPERATER: FORM
SOFTWARE: WOYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-0ct-1998
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 15 US-09-165-546D-15
                                       Sequence 15, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                    US-09-165-546D-15
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Wolf, Greenfield & Sacks, P.C.
                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAWE: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFRENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.5%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 210 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 91.7
Matches 11; Conservative
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51 ARASGPRGGAPR 62
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51 ARASGPRGGAPR 62
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                                                                              ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         linear
    ADDA.
STREET: 60.
                                                                USA
                                                            COUNTRY: U
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-341-829A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.5%; Score 56; DB 1; Length 180; Best Local Similarity 91.7%; Pred. No. 2.3; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%; Score 56; DB 2; Length 180; 91.7%; Pred. No. 2.3; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Locas, Sophie
APPLICANT: De Smer, Charles
APPLICANT: Godélaine, Daniele
TITLE OF INVENTION: Li-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
APPLICALL...
RILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGIGSTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-341
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLLOGY: linear
TOPOLLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                            1 ARASGPGGGAPR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-341-829A-7
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US-08-791-495-5
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Fatent No. 6794131
GENERAL INFORMATION:
APPLICANT: Leth., Bernard
APPLICANT: Lot. Sophie
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Indee 1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REPERRENCE: Lot. 1999-10-18
CURRENT FILLING DATE: 1999-10-18
CURRENT FILLING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495
PRIOR APPLICATION NUMBER: PCT/US99/01445
C151> 1999-01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 2; Length 210;
Pred. No. 2.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 1; Length 210;
Pred. No. 2.7;
0; Mismatches 1; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 210
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-08-789-329C-10

| Sequence 10. Application US/08789329C |
| Patent No. 6165755 |
| Patent No. 6165755 |
| GENERAL INFORMATION: |
| APPLICANT: SHERWOOD ET AL. |
| TITLE OF INVENTION: POR IMPROVED POULTRY PRODUCTION UNDER OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: Whinston, LLP |
| STREET: One World Trade Center STREET: One World Trade Center STREET: Suite 1600 |
| CITY: Portland STRAE: Oregon |
| COUNTRY: United States of America |
| STREET: Suite 1600 |
| CITY: Portland |
| STREET: Suite 1600 |
| CITY: Portland |
| STREET: Suite 1600 |
| CITY: Portland |
| STREET: Suite 1600 |
| CITY: Portland |
| STREET: Suite 1600 |
| CITY: Portland |
| STREET: Suite 1600 |
| CONDUTER: READABLE FORM: |
| MEDIUM TYPE: Disk, 3-1/2 inch |
| COMPUTER: IBM FC compactible |
| CORPUTER: IBM FC compactible |
| COMPACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 2;
Pred. No. 97;
                                                                                                                                              FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31759
LENOTH: 8099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759
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INFORMATION FOR SEQ ID NO: 10:
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81.8%;
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Matches 9; Conservative
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                                                                                                                                                                                           APPLICANT: Ramensee, Hans Georg
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: Gene, and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-26
PRIOR PELLOR DATE: 1998-06-26
PRIOR PELLOR DATE: 1998-06-26
PRIOR PILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 17
LENGTH: 9
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Fatent No. 6673350

GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Bahin, Ugur
APPLICANT: Pireundachuh, Michael
APPLICANT: Pireundachuh, Michael
APPLICANT: Pireundachuh, Michael
APPLICANT: Pireundachuh, Michael
APPLICANT: Prueci, Ozlem
APPLICANT: Pireundachuh, Michael
FILE REFERENCE: LUD 5622.1
CURRENT FILING DATE: 1099-06-25
PRIOR PILING DATE: 1999-06-26
PRIOR PELING DATE: 1999-06-26
PRIOR PELING DATE: 1999-06-26
PRIOR PELING DATE: 1999-06-26
PRIOR PELING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE PETENTIN Version 3.2
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US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
                      Sequence 117, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahim, Ugur
APPLICANT: Pfreundschuh, Michael
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Best Local Similarity 100.
Matches 9, Conservative
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Best Local Similarity 100..
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US-09-833-039A-117
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US-09-344-040C-117
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Query Match
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 2 RASGPGGGAPR 12
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2 RASGPGGGAPR 12 || || || || 56 RAGAPGGGGPR 66

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Search completed: March 13, 2006, 19:18:52 Job time : 23.3059 sec8

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial
                  JS-10-296-734-1404
LENGIH:
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i, Appl
i, Appl
Appli
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Sequence 14, Appl
Sequence 3, Appli
Sequence 74, Appl
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7, Appli
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Sequence 30, Appli
Sequence 8, Appli
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Sequence 386, A
Sequence 832, A
Sequence 139, A
Sequence 11, Api
                                                                March 13, 2006, 19:51:56; Search time 72.5647 Seconds (without alignments) to 69.096 Million cell updates/sec
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Sequence 7
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-849-602-30

US-10-023-188-8

US-10-207-655-71

US-10-364-614-14

US-10-364-614-14

US-10-1026-66-3

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-295-724-832

US-10-871-711

US-10-877-721-11

US-10-877-71-11

US-10-877-71-11

US-10-877-71-11
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US-11-067-064-74
US-11-067-159-74
US-09-821-883-27
US-11-144-912-27
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                  1867569 segs, 417829326 residues
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                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                      US-09-529-206E-29
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Maximum DB seq length: 200000000
                                                                                                                               1 ARASGPGGGAPR 12
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Match Length
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Perfect score:
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; Publication No. US20040054137A1
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Rambhaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE OF INVENTION: Synthetic molecules and uses therefor CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR PPLICATION NUMBER: AU PQ7761/00
; PRIOR PILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patentin version 3.2
; ENGTH: 30
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US-10-296-734-1436
US-10-295-027-388
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US-10-1146-473-69
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US-10-296-734-834
US-10-296-734-834
US-10-657-022-75
US-11-067-028-75
US-11-067-038-88
US-10-117-937-76
US-10-657-022-76
US-10-657-022-76
US-10-657-022-76
US-11-067-084-76
US-11-067-084-76
US-11-067-084-76
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US-11-067-084-76
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; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
    APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; TILE REFERENCE: P 573 PCOO
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 202
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: NYSOla segment 4
US-10-296-734-1404
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Stockert, Elisabeth
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                                                   Gaps
                                                                                                                                                                                                                                                                                              APPLICANT: Stocker, Elisabeth, Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Truncated Proteins, Uses Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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    100.0%; Score 64; DB 5; Length 179; 100.0%; Pred. No. 0.93; ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 'Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. US2002010321Alman D. REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
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Patent No. US20020010321Al
GENERAL INFORMATION:
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Query Match
Best Local Similarity 100.
Matches 12; Conservative
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TOPOLOGY: linear
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Sequence 30, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.

US-09-849-602-30

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Gaps
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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: 1B4
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. US20020164665Alman D. REGISTRATION UNBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York
COUNTRY: USA
APPLICANT: Chen, Yao-reeng
TITLE OF INVENTION: COlon Cancer Antigen Panel
FILE REPERBENCE: L046/1/105 (URV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: AUNHOWER: 08/725,182
PRILING DATE: CUNHOWNP.
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US-10-023-182-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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US-09-849-602-30
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                              APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: BRITOPE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFRENCE: CTLIMM.21CPI
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT APPLICATION NUMBER: 09/561,074
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
PRIOR PRI
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PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR PRILING DATE: 2001-04-06
PRIOR PRILING DATE: 2001-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 74, Application US/10117937
Publication No. USZ0030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.0274
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
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Best Local Similarity 100...
Best Local 2; Conservative
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Matches 12; Conservative
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Sequence 14, Application US/10364614

Sequence 14, Application US/10364614

Sequence 14, Application US/10364614

Sequence 11, Application No. US/2030175250A1

SERBEAL INFORMATION:

APPLICANT: CAUTY, Alexander

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILLE REPRENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION WUMBER: US 60/355,828

PRIOR PILLING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                           Sequence 71, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
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100.0%; Score 64; DB 4; Length 180;
100.0%; Pred. No. 0.94;
ive 0; Mismatches 0; Indels
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; Publication No. US20030215425A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                     Best Local Similarity 100.
Matches 12; Conservative
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51 ARASGPGGGAPR 62
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US-10-207-655-71
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LENGTH: 180
TYPE: PRT
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      Query Match
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LENGTH: 180
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                                                                                                                   APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Afar, Matasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glyb, Kurt C.
APPLICANT: Glyb, Kurt C.
APPLICANT: Glyb, Kurt C.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Wateon. Susan R.
APPLICANT: Sus
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US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT APPLICATION NUMBER: AU PQ7761/00
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SEQ ID NO 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 64; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 0.94; Matches 12; Conservative 0; Mismatches 0; Indels
                          Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
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LENGTH: 180
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US-10-188-832-139

i Sequence 139, Application US/10188832

i Eublication No. US20040076955A1

GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Application Set Softechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US

CURRENT FILING DATE: 2002-11-22

PRIOR FILING DATE: 2001-00-03

PRIOR PLICATION NUMBER: US 60/302,814

PRIOR FILING DATE: 2001-00-03

PRIOR FILING DATE: 2001-00-03

PRIOR FILING DATE: 2001-11-03

PRIOR FILING DATE: 2001-11-03

PRIOR FILING DATE: 2001-11-03

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 207

SPOTTAMER: PATECHTIN VET: 2.1
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Sequence 11, Application US/10777053
Publication No. US20040132088A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REPERENCE: MANNK. 02.2C1
CURRENT APPLICATION NUMBER: US/10/777, 053
CURRENT FILING DATE: 2004-02-10
PRIOR PILING DATE: 2002-11-07
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; Pred. No. 0.94;
0; Mismatches 0; Indels
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                                                                                     ; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832
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                                                                                                                                                    Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                        1 ARASGPGGGAPR 12
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CORGANISM: Homo sapiens
US-10-188-832-139
TYPE: PRT
ORGANISM: Artificial
FEATURE:
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Sequence 74, Application US/10657022

Publication No. US20040180354A1

GRENEAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNER: 0324
CURRENT PELING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: 60/409123

PRIOR PILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610

SOFTWARE: FASEEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74
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Best Local Similarity
Matches 12; Conserva
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Sequence 15, Application US/10751088
Publication No. US20040158044A1
GENERAL INFORMATION:
APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLUSES THEREOF
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER. IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION NUMBER: US/09/165,546D
FILING DATE: 02-OCT-1998
APPLICATION NUMBER: US/09/165,546D
FILING DATE: April 17, 1998
APPLICATION NUMBER: US/09/165,546D
FILING DATE: April 17, 1998
APPLICATION NUMBER: US/08/122
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/08/37,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/08/725,182
FILING DATE: September 15, 1996
APPLICATION NUMBER: US/08/725,182
APTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: UD/02166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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100.0%; Score 64; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                  PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SEQ ID NO 11
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear;
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15
PRIOR APPLICATION NUMBER: 60/336,968
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                              1 ARASGPGGGAPR 12
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                                                                                                                                                 TYPE: PRT
CORGANISM: Homo Sapien
US-10-777-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-751-088-15
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RESULT 2
US-11-021-441-28
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SEQ ID NO 7
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Sequence 496, Appl
Sequence 20556, A
Sequence 2395, Ap
Sequence 22317, A
Sequence 22333, A
Sequence 27265, A
Sequence 27265, A
Sequence 27265, A
Sequence 27265, A
Sequence 2332, A
Sequence 2332, A
Sequence 38, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 66, Appl
Sequence 14, Appl
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Sequence 2722, Ap
Sequence 58, Appl
Sequence 1240, Ap
Sequence 8, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    March 13, 2006, 19:54:06; Search time 8.18824 Seconds (without alignments) 40.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Ap
Sequence 2, Ap
Sequence 54, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-155-288-7
US-11-021-441-28
US-10-623-155-496
US-11-096-568A-20556
US-11-096-568A-20310
US-11-096-568A-22331
US-11-096-568A-22331
US-11-096-568A-22331
US-11-096-568A-22331
US-11-096-568A-22331
US-11-1096-568A-22331
US-11-072-512-3369
US-11-240-769-58
US-11-240-769-58
US-11-240-769-58
US-10-922-577-8
US-11-223-294-54
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       161667 seqs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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64
                                                                                                                                                                                                                                                               1 ARASGPGGGAPR 12
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Match Length DB
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Perfect score:
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                                                                                               OM protein
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                                                                                                                                        Run on:
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No.
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26 39 60.9 618 7 US-11-078-735-18 Sequence 18, Appl 29 60.9 618 7 US-11-050-346-63 Sequence 63, Appl 29 60.9 618 7 US-11-013-077-18 Sequence 18, Appl 30 60.9 66.9 7 US-11-013-077-18 Sequence 18, Appl 30 60.9 66.9 7 US-11-013-077-18 Sequence 18, Appl 31 32 86.9 836 7 US-11-072-105 Sequence 197, Appl 32 85.4 132 7 US-11-096-568-1390 Sequence 197, Appl 33 34 38 59.4 162 7 US-11-096-568-1413 Sequence 14323, Appl 36 59.4 162 7 US-11-096-568-1457 Sequence 14323, Appl 36 59.4 235 7 US-11-096-568-1457 Sequence 1070, Appl 37 38 59.4 235 7 US-11-096-568-1457 Sequence 22663, Appl 38 59.4 236 7 US-11-096-568-12695 Sequence 22603, Appl 39 38 59.4 236 7 US-11-096-568-12070 Sequence 22603, Appl 39 39 59.4 236 7 US-11-096-568-12071 Sequence 22603, Appl 39 59.4 236 7 US-11-096-568-12071 Sequence 22603, Appl 41 38 59.4 274 7 US-11-096-568-12071 Sequence 22603, Appl 42 38 59.4 4 438 6 US-10-081-234-1628 Sequence 1628, Appl 44 38 59.4 4 438 6 US-10-921-793-38 Sequence 9 Appl 144 38 59.4 4 438 6 US-10-921-793-38 Sequence 38, Appl
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## ALIGNMENTS

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| USE | USE
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Gaps

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Sequence 23806, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 23806
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 134;
                                                                                                                                                                                                              Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                            Score 47; DB 7;
Pred. No. 9.5;
0; Mismatches
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Pred. No. 6.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1).7(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806
                                                                                                                  ; LOCATION: (1)...(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGARARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11.072-512-3295

Sequence 3295, Application US/11072512

Publication No. US20060029945A1

GENERAL INFORMATION:
                              TYPE: PRT ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays subsp. mays
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SATO, HIROYUKI
ISHII, SHIZUKO
YAWAWOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.9%;
72.7%;
                                                                                                                                                                                                                73.4%;
81.8%;
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OTSUKI, TETSUJI
                                                                                                                                                                                           Query Match
Best Local Similarity 81.0-
Best Local Similarity
Secondary
Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                        91 ARADGPGTGAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                         1 ARASGPGGGAP 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ARGAGPGAGAP 79
                                                                      FEATURE:
NAME/KEY: misc_feature
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US-11-096-568A-20556
US-11-096-568A-20556
Sequence 20556, Application US/11096568A
Foreign No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Reangef, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REPERBENCE: 210121.455520
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT PILLIG DATE: 2003-07-17
NUMBER OF SEG ID NOS: 560
SOFTWARE: FRREESQ for Windows Version 4.0
SEG ID NO 496
LENGTH. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 64; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.2%; Score 52; DB 6; Length 20;
100.0%; Pred. No. 0.19;
tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PRILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-05
PRIOR FILING DATE: 2004-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR PILING DATE: 2004-03-26
PRIOR PILING DATE: 2004-03-26
SOFTWARE: FASCEQ for Windows Version 4.0
SEQ ID NO 28
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-623-155-496
Sequence 496, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Fusion protein
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 ARASGPGGGAPR 122
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Matches 10; Conservative
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Gaps

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US-11-096-568A-22333

Sequence 22333, Application US/11095568A

Sequence 22333, Application US/11095568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1522F032

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-096-568A-27265
US-11-096-568A-27265
Sequence 27265, Application US/11096568A
Sequence 27265, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Allacandrow, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27265
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                                                                                 Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Length 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                            Indels
                                                                                 Score 43; DB 7;
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | LOCATION: (1). 7 (413)
| OTHER INFORMATION: Ceres Seq. ID no. 15180691
| US-11-096-568A-27265
  ; LOCATION: (1)...(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1). (358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333
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Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                   66.78;
                                                                                                                                                                                                         109 ARGQGPGGEQPR 120
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Best Local Similarity 66...
8; Conservative
                                                                                 Query Match 67.2
Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8, Conservative
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Publication No. US20060048240A1
GENERAL INFORMATION:
FULL INFORMATION:
FILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 558
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Sequence 22334, Application US/11095568A

Fublication No. US2060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE REPREBLOCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 22334
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                                                                                                                                                                                                                                                                                                              Score 45; DB 7; Length 678;
Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                      1; Indels
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Pred. No. 41;
0; Mismatches
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US-11-096-568A-26217
                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
              CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION, UMBER: UP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3295
LENGTH: 678
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                                                                                                                                                                                                                                                                                                              70.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.8%;
ilarity 66.7%;
Conservative
FILE REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 ARQEGPAGGEPR 400
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0
Matches 8; Conservative
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592 RAAGPGGGWP 601
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US-11-072-512-3295
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Best Local Similarity
Matches 8; Conserv
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 7; Length 537; Pred. No. 99; 2; Indels
Publication No. US20060030537A1;
GENERAL INFORMATION:
APPLICANT: Chalfant, Charles E.
APPLICANT: Hannun, Yuesf A.;
APPLICANT: Hannun, Yuesf A.;
APPLICANT: Bielawska, Alicja
TITLE OF INVENTION: Ceramide Kinase and Uses Thereof;
FILE REFERENCE: 9175-028-999 (WUSC Ref P0401);
CURRENT FILING DATE: 2005-07-11;
FRIOR APPLICATION NUMBER: 60/586,909
FRIOR PILING DATE: 2004-07-09;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
IEBNGTH: 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 084335-0191
CURRENT PAPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2011-11-05
                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Human ceramide kinase US-11-179-958A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3369, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3369
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RASGPGGGAP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 RSPGPGAGAP 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Homo sapiens
US-11-072-512-3369
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                           Sequence 2332, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22332
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Laterin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Mary Elizabeth
APPLICANT: Wang, Elizabeth
APPLICANT: Shamah, Steven M.
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CURRENT APPLICANTON: METHODS OF PROMOTING CURRENT APPLICANTON NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
| LOCATION: (1):7(420)
| TOTER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58, Application US/11108528; Publication No. US20050261189A1; GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/11179958A
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Matches 8; Conservative
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US-11-108-528-58
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LENGTH: 365
TYPE: PRT
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US-11-108-528-58
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US-11-179-958A-2
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3 ASGPGGGAP 11

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Search completed: March 13, 2006, 20:03:31 Job time : 8.18824 secs

214 GPGGGHPR 221

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(without alignments)
58.355 Million cell updates/sec
                                                                                                         March 13, 2006, 18:52:59; Search time 82.8235 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DB	ID	Description
-	09	100.0	11	7	AAY06066	Aay06066 Human can
7	9	100.0	12	~	AAY06065	
٣	9	100.0	13	7	AAY06064	Human
4	9	100.0	14	8	AAY05986	_
Ŋ	9	100.0	15	~	AAY05978	_
9	9	100.0	20	7	AAY05979	_
7	9	100.0	30	S	AAU85105	Aau85105 Human NYN
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10	9	100.0	180	~	AAW69665	Aaw69665 Human NY-
11	9	100.0	180	7	AAY05965	Aay05965 Human can
12	9	100.0	180	m	AAY52430	Aay52430 Human tum
13	9	100.0	180	ო	AAY70862	Aay70862 Human tum
14	9	100.0	180	٣	AAB03154	Aab03154 Human oes
15	9	100.0	180	4	AAB69946	Aab69946 Human NY-
16	9	100.0	180	4	AAG67164	Aag67164 Amino aci
17	9	100.0	180	4	AAU01535	Aau01535 Human NY-
18	9	100.0	180	4	AAE07714	Aae07714 Human NY
19	9	100.0	180	ß	AAU84818	Aau84818 Human NYN
20	9	100.0	180	ហ	AAU11543	Aau11543 Human tum
21	9	100.0	180	9	ABR58672	Abr58672 Human can
22	9	100.0	180	9	ABR48210	Abr48210 Human bla
23	9	100.0	180	9	ABU56508	Abu56508 Lung canc
24	9	100.0	180	9	ABU56694	Abu56694 Lung canc

Abp74198 Human NY- Abu64816 Human NY- Abr89438 Human NY- Adc09576 NY-ESO-1		Adm72815 Human NY-Adm72815 Human NY-Adm73417 Human NY-Adg18451 Human sof Add10446 Autoimmun	
ABP74198 ABU64816 ABR83438 ADC09576	ADD35564 ADD35568 ADD25510 ADN39068	ADM73415 ADM73418 ADM73417 ADQ18451 ADQ10446	ADS80926 ADW44353 ADY85096 ADZ28913 ADZ42374 AEA35651 ADW99402
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## ALIGNMENTS

RESULT 1

This peptide corresponds to amino acid residues 52-62 of human NY ESO-1/CAG-3 ORP1 (see AAY05965), a new and potent tumour antigen that is expable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-lodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; carcer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic I lymphocyte; CTL. Human cancer antigen NY ESO-1/CAG-3 peptide. (USSH ) US DEPT HEALTH & HUMAN SERVICES. Example 11; Page 50; 88pp; English. AAY06066 standard; peptide; 11 AA. Cancer antigen NY ESO1/CAG-3. 98WO-US019609. 97US-0061428P. (first entry) Wang RF, Rosenberg SA; WPI; 1999-277270/23. WO9918206-A2. 21-SEP-1998; 08-OCT-1997; Homo sapiens 15-APR-1999. 16-AUG-1999 AAY06066; AAY06066 

cancer;

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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; terine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CTL.
                                                                                                                                     Human cancer antigen NY ESO-1/CAG-3 peptide.
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                                                      AAY06064 standard; peptide; 13 AA
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cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide corresponds to amino acid residues 51-62 of human NY ESO-
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                                                                                                                                                                                                                                                                                                                                        leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic I lymphocyte; CTL.
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                                                                    2; Length 11;
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0.14;
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                                                                  100.0%;
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                                       This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CAG-3 ORPI (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an Hish molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                    as breast, prostate, ovarian, pancreatic and thyroid cancers
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Pred. No. 0.16;
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Example 11; Page 50; 88pp; English.
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RASGPGGGAPR 12

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The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of elicting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their capables (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods (or preventing or inhibiting cancer by administering a cancer peptide, which molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carcines such as primary or metastatic melanoma, thymoma, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
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NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breate cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
                                                                                                    liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer antigen NY ESO1/CAG-3.
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                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 AA;
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                  WO9918206-A2
                                                                                                                                                                                                                                                                                21-SEP-1998;
                                                                                                                                                                                                                                                                                                                     08-OCT-1997;
                                                                                                                                                                                                                                       15-APR-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                   Wang RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The present sequence represents a cancer peptide that corresponds to amino acid residues 48-62 of human BSO-1/CAG-3 (or CAG-3) ORF1 (see AAV05956), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAV05966), portions of them and their cancer specimes that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a cransgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide or tumour antigen; antibodies reacting with a cCAG-3 cancer peptide or tumour antigen; antibodies reacting with a cCAG-3 cancer peptide, useful in diagnostic and detection assays; and methods concer peptide, useful in diagnostic and detection assays; and methods concer peptide or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastetic melanoma, thymoma, cancer bladder cancer, liver cancer, leukaemia, uterine cancer, lymphoms, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, panceatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; non-Hödgkins lymphoma; Hödgkins lymphoma; lung cancer; metaatasis; melanoma; adenocarcinoma; thymoma; colon cancer; netrine cancer; breast cancer; prestate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; paroreatic cancer; liver cancer; parcoma; therapy; therapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 60; DB 2; Length 15; 100.0%; Pred. No. 0.18; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05979 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 64; 88pp; English.
                                                                                                                                                                                                                                                             97US-0061428P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer antigen NY ESO1/CAG-3.
                                                                                                                                                                                                                     98WO-US019609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RASGPGGGAPR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                 Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 RASGPGGGAPR
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                        Homo sapiens
                                                                                                                              WO9918206-A2
                                                                                                                                                                                                                                                           08-OCT-1997;
                                                                                                                                                                                                                  21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-1999
                                                                                                                                                                          15-APR-1999.
  cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY05979;
                                           vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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25-MAY-2001; 2001WO-AU000622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                       Thomson SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK68648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK68648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-3 ORF2 (see AAY05966), portions of them and second them and their cancer and detection assays; and methods in an integer, antibodies reacting with a CAG-3 cancer peptide, or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, unbibiting cancer by administering a cancer peptide, with or without an cancer such as primary or metasetaic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancers bladder cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, panoreatic and thyroid cancers. Melanoma is treated by an interval and interval of the subsequent return to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 60; DB 2; Length 20; 100.0%; Pred. No. 0.23; ive 0; Mismatches 0; Indels
                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU85105 standard; peptide; 30 AA.
                                                                                                                                                                                                                          Claim 16; Page 64; 88pp; English.
                                                                                                                                                                                                  Cancer antigen NY ESO1/CAG-3.
                                                                                  98WO-US019609
                                                                                                        97US-0061428P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NYNSOla segment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 RASGPGGGAPR 20
                                                                                                                                                     Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RASGPGGGAPR 11
                                                                                                                                                                             WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                       08-OCT-1997;
 Homo sapiens
                                   WO9918206-A2
                                                                                  21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2001
                                                          15-APR-1999
              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU85105;
                                                                                                                                                     Wang RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relativathy relative to their linkage in the together in a different relativathy relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polymetic polymetides. The synthetic polypeptides and polymetide synthetic polypeptides. The synthetic polypeptide are a savine. The synthetic polypeptide is useful for a referred to as a Savine. The synthetic polypeptide is useful for a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head can neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oseophagus, brain, testicle, uterus), as potentiating agents.

C cancer, (e.g., rania, testicle, uterus), as potentiating agents.

C compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human comprising the polypeptide may be used in the treatment or prophylaxis against virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, colons almonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Teishmania, construct a savine of the instrict and parent protein used to construct a savine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                    New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitope liberation; substrate; proteasome; cytostatic; antibacterial; protezoacide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epitope liberation-related NY-ESO-1 protein SegID11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK68648 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 27; 364pp; English
26-MAY-2000; 2000AU-00007761.
                                                                                       (AUSU ) UNIV AUSTRALIAN NAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RASGPGGGAPR 11
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                                                                                                                                                                                                                                                                                         WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Bite" site"

(SIMA/) S (DIAM/) I (QIUZ/) C (LEIX/) I

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The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an NHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 60; DB 2; Length 180; 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gure A, Old LJ, Jager E, Knuth A;
                                                                        note= "potential myristorylation site"
                                                                                                                                                                                                                                                            /note= "potential phosphorylation site"
                            note= "potential myristorylation site"
                                                                                                                                                                                                               'note= "potential phosphorylation site"
                                                                                                                                                                   'note= "potential phosphorylation
                                                                                                                     'note= "potential phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 3; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US016335.
                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00725182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-286417/25.
                                                                                                                                                                                       Misc-difference 134
                                                                                                                                                                                                                                    Misc-difference 138
                                                                                                                                           Misc-difference 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic regime
                                                                                             Misc-difference 11
       Misc-difference 7
                                                  Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV38566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drijfhout JW;
                                                                                                                                                                                                                                                                                                          WO9814464-A1
                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-0CT-1998
                                                                                                                                                                                                                                                                                                                                                     09-APR-1998.
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       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying an epitope of interest; providing substrate polypeptide sequence including the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome; contacting the substrate with a composition including the proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, proteasome of compounds with a cytostatic, antibacterial, contaction may allow development of a vaccine. The invention contaction may allow development of a vaccine. The invention contaction may allow development of a vaccine. The invention contaction may allow development of a vaccine. The invention may allow development of a vaccine. The invention contaction may allow development or in the generation or expansion of cytotoxic T lymphocyte contaction in a doptive immunotherapy. The invention is also useful contactivating T-cells against neoplastic cells, and cells infected with cyirus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the consection proteasome system. Once identified, these epitopes, embodied as peptides, can be used to successfully immunise or induce therapeutic CTL responses against housekeeping proteasome expressing traget cells in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                    Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 60; DB 8; Length 179; 100.0%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                        Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW62584 standard; protein; 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                        Qiu Z,
                                             07-NOV-2002; 2002US-00292413.
                                                                                         07-NOV-2001; 2001US-0336968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1998 (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                        Simard JJL, Diamond DC,
                                                                                                                             ) DIAMOND D C.
) QIU Z.
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                                                                                                                                                                                                                                                                                                   2004-167209/16.
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N-PSDB; ADK68674
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11-DEC-2003
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Gaps

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Ното варіеля W09832855-A1

Location/Qualifiers

Homo sapiens

Key

AAW62584;

RESULT 9

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The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and content tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAY05966), portions of these peptides and their variants (see AAY05965).

CAAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), portions of these peptides and their variants (see AAY05965-CC AAY05966), a method of diagnosis of cancer or precancer; catenoment of cancer. The intention provides: vectors and host cells catenoment of animal; antisense oligonucleotides that inhibit expression of the cancer peptide, useful in diagnostic and detection assays; and methods of preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carcoma, lung cancer, liver cancer, leukaemia, uterine cancer, lymphoma, sarcoma, lung cancer, liver cancer and adenocarcinomas such as breast, prostate, ovarian, panceraetic and thyroid cancers. Melanoma is tranted by inducing cancer, specific T cells in vitro for subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytotoxic; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60. .68
/note= "Peptide presented by MHC Class I HLA-B7"
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                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 3A; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                    Cancer antigen NY ESO1/CAG-3.
                                                                         97US-0061428P
                          98WO-US019609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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/note= "
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                                                                                                                                                                       Wang RF, Rosenberg SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                                                                                                                                                                                              WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            return to a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                     N-PSDB; AAX58599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 180 AA;
                          21-SEP-1998;
                                                                      08-OCT-1997;
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Unidentified.
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15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes LAGE-1 tumour associated protein (TAP). The present invention also describes (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for cells with an agent presenting a complex of a LAGE-1 TAP or an isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                            New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                    Godelaine D,
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 57-58; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05965 standard; protein; 180 AA.
                                                                                                                                                                                                    De Smet C,
                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                97US-00791495.
                                                 98WO-US001445
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                particularly tumours.
                                                                                                                                                                                                                                                     WPI; 1998-427951/36.
                                                                                                                                                                                                    Lucas S,
                                                                                                                                                                                                                                                                             N-PSDB; AAV50348.
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                                                 27-JAN-1998;
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30-JUL-1998
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RESULT 11

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(BOEH ) BOEHRINGER INGELHEIM INT GMBH. (UYHO-) UNIV HOSPITAL LEIDEN.
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                                                          WPI; 2000-038483/03
                                  E, Jager
Ritter G;
                                                                  N-PSDB; AAZ38380
                                                                                                                                                                                                                                                                                                          Sequence 180 AA;
 02-OCT-1998;
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                                   Stockert
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                                           Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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/note= "Peptide presented by MHC Class I HLA-A24 and HLA-
                                                                                                                                                                                                                                                113. .122
/note= "Peptide presented by MHC Class I HLA-B7 and HLA-B52"
B52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-
                                        by MHC Class I HLA-B7, HLA-B8
                                                                                                           84. .92
/note= "Peptide presented by MHC Class I HLA-B7, HLA-B9
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/note= "Peptide (AAY52434) presented by MHC Class I
                                                                                         .91
.e= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                  88. .96
/note= "Peptide presented by MHC Class I HLA-B44"
                                                                                                                                                                                                       /note= "Peptide presented by MHC Class I HLA-B44"
107. .116
                                                                                                                                                                                             /note= "Peptide presented by MHC Class I HLA-B44"
102. .110
                                                                                                                                                                                                                                                                                                                                                     note= "Peptide presented by MHC Class I HLA-A24"
138. 147
                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Peptide presented by MHC Class I HLA-B52"
[54. .163
                                                                                                                                                                                                                              /note= "Peptide presented by MHC Class I HLA-A24"
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                                                                                                                                                                                                                                                                                                                                          note= "Peptide presented by MHC Class I HLA-B52"
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/note= "Peptide presented by MHC Class I HLA-B52"
                                                                                                                                                                                                                                                                                113. .121
//note= "Peptide presented by MHC Class I HLA-B7"
115. .124
//note= "Peptide presented by MHC Class I HLA-A3"
118. .126
                       presented by MHC Class I HLA-87"
                                                                                  presented by MHC Class I HLA-A1"
                                                                                                                                            "Peptide presented by MHC Class I HLA-Al"
                                                                                                                                                                            /note= "Peptide presented by MHC Class I HLA-B7"
100. .108
                                                                                                                                                                                                                                                                                                                                                                                   139. 147
'note= "Peptide presented by MHC Class I HLA-B7"
                                                                                                                                                                                                                                                                                                                                                                           'note= "Peptide presented by MHC Class I HLA-B8"
        "Peptide presented by MHC Class I HLA-B7"
                                                                  "Peptide presented by MHC Class I HLA-A1"
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                        "Peptide
                                        "Peptide
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                                                                                                                            and HLA-B35"
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                                                  HLA-B35
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                                                                                                                                                                                                                                       110. .118
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               .88
                                 . 87
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This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer CDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY -ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class II molecules for presentation to T-cells. Peptides AAV52431- V52434 bind to Class I HAA-2 molecules, thereby stimulating proliferation of cytotoxic T-cells, while peptides AAV52455-Y5240 bind to Class II HIA-DR53 molecules, stimulating helper T-cell proliferation. The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL; cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer; melanoma; immunotherapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Revised record issued on 21-OCT-2004 : Correction to feature table key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes.
                                                                                                                                                                              old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                   Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour antigen, NY-ESO-1 protein.
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                                                                                                                                                                                   Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Fig 3; 49pp; English.
                                                                                              (LUDW-) LUDWIG INST CANCER RES
98US-00165546.
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03-OCT-1996;
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                                                                            Scanlan M,
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                                                                                         01d LJ;
                                           (CORR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                   The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an esophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF)—I that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytoroxic T lymphocytes (CTL)—recognised Antigen on MELanoma) protein, a tumour-associated antigen. The tumour-associated antigen of displayed on melanoma cells is recognised by cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or
                                                              Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen; oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.
                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                      100.0%; Score 60; DB 3; Length 180; 100.0%; Pred. No. 1.5; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Potential O-phosphorylation site"
152. .172
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Potential O-phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Potential O-phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human oesophageal cancer-associated antigen NY-ESO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Potential O-phosphorylation
         Klade C;
         Heider K,
                                                                                                  Example 3; Page;62-63; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB03154 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                   1 Similarity 100.0%;
11; Conservative 0
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         Aarnoudse CA,
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                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                     1 RASGPGGGAPR 11
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                               WPI; 2000-339685/29
                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 11; Conserv
                                          N-PSDB; AAD00152
                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                                                                                                                                                                                                              fusion proteins
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         Schrier PI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB03154;
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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This sequence represents a human oesophageal cancer-associated antigen, NY-ESO-1. The CDNA encoding this sequence was isolated from a CDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophageal Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue, but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, ceveral N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The artigen is useful as an immunogen when combined with an adjuvant, in both correctsor and post- translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targetted delivery of therapeutic agents to besophageal cancer cells. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                    Sahin U, Pfreundschuh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 60; DB 3; Length 180; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Chen Y, Tureci O,
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(SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                             (SLOK ) SLOAN KETTERING INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 3; 9pp; English.
                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
96US-00725381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. infections and cancer.
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                                                                                                                          CORNELL RES FOUND
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                                                                                                                                                                                                                                    Gure AO,
                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-410880/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA61483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180 AA;
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(CORR ) CORNELL RES FOUND INC
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Knuth A, Chen Y, Scanlan M; old LJ, Jager E, Stockert E,

WPI; 2001-182822/18.

N-PSDB; AAF58634.

Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

Example 5; Fig 3; 50pp; English.

The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for efermining whether a cancerous condition is progressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder 

Sequence 180 AA;

100.0%; Score 60; DB 4; Length 180; 100.0%; Pred. No. 1.5; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 11; Conservative Query Match

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Gaps .; 0

1 RASGPGGGAPR 11

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52 RASGPGGGAPR 62

Search completed: March 13, 2006, 19:04:00 Job time : 83.8235 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

March 13, 2006, 19:04:24; Search time 13.0706 Seconds (without alignments) 80.975 Million cell updates/sec

US-09-529-206E-30 60 1 RASGPGGGAPR 11 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lisking first 45 summaries

PIR 80:* Database

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOUTHERNIES	
Result No.	Score	Query	Length	DB	Ω	Description
-	44	73.3	3190	2	T13828	CREB-binding prote
8	42	70.0	351	~	S50754	
е	42	70.0	378	~	C87425	₽
4	41	68.3	173	~	AB3648	flagellar basal-bo
ហ	41	68.3	286	7	804673	H+-transporting tw
9	41	68.3	357		F82878	XAA-PRO aminopepti
7	41	68.3	1207		T00378	KIAA0641 protein -
œ	40	66.7	335		S08341	myristylated alani
6	40	66.7	371		T39312	hypothetical prote
10	40	66.7	383		A86182	
11	40	66.7	436	~	T36104	conserved hypothet
12	40	66.7	521	~	A29345	steroid hormone re
13	40	66.7		~	S02165	regulatory protein
14	40	66.7		7	A87431	regulatory protein
15	39	65.0		~	C72683	hypothetical prote
16	39	65.0		7	B45036	Pur beta - human (
17	39	65.0		~	E87464	competence/damage-
18	39	65.0		N	169006	histocompatibility
19	39	65.0	187	~	T35619	hypothetical prote
20	39	65.0		7	F95899	probable transcrip
21	39	65.0	307	7	B72677	hypothetical prote
22	39	65.5		~	T52451	endopeptidase Clp
23	39	65.0		~	F95307	conserved hypothet
24	39	65.0		7	G75580	conserved hypothet
25	39	65.0	266	~	T34842	probable transfera
26	39	65.0	575	7	835327	protein kinase sgg
27	39	65.0	620	~	T30765	hypothetical prote
28	39	65.0	627	~	T35608	polyketide hydroxy
59	39	65.0	733	7	S10932	probable protein k

transducin-like en	(1->4)-alpha-D-glu	hypothetical prote	DNA-binding protei	protein kinase sgg	ovo protein - frui	apoptosis associat	calo protein - fru	hypothetical prote	hypothetical prote	Pex-related protei	peptidyl-tRNA hydr	peptidyl-tRNA hydr	anther-specific pr	hypothetical prote	Hypothetical Prote
C56695	JC7726	807132	A56038	835423	S16356	T03748	T13719	C72637	C87270	C75445	H87399	AH3506	S12246	T36874	AE3136
~	N	N	N	N	0	~	0	N	7	~	N	~	~	0	7
743	757	886	1028	1067	1213	1317	4116	104	112	131	143	145	191	185	189
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C; Accession: T13828
R; Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gs
R; Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gs
R; Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gs
R; Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gs
A; Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A; Reference number: Z17785; MUID:97263578; PMID:9109493

A,Accession: T13828
A,Batus: preliminary; translated from GB/EWBL/DDBJ
A,Rolecule type: mRNA
A,Rosiques: 1-3190 <AKX>
A,Coss-references: UNIPROT:001368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; P

A;Cross-references: FlyBase:FBgn0015624 A;Map position: X F;1723-1780/Domain: bromodomain homology <BRO>

Gaps ö Query Match 73.3%; Score 44; DB 2; Length 3190; Best Local Similarity 77.8%; Pred. No. 2.3e+02; Matches 7; Conservative 1; Mismatches 1; Indels

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320 NGPGGGGPR 328 3 SGPGGGAPR 11 δ 음

Nypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: A-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754
A;Reference number: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: S50754
A;Accession: L351
A;Accession: L351
A;Accession: C;Accession: C;Ac

ö 70.0%; Score 42; DB 2; Length 351; 80.0%; Pred. No. 69; ive 0; Mismatches 2; Indels Query Match
Best Local Similarity 80.0
Matches 8, Conservative

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Gaps

299 RASPPGGGPP 308 1 RASGPGGGAP 10 셤 ઠ

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A,Molecule type: DNA
A,Residues: 1-286 <TYB>
A,Cross-references: UNIPROT:P05436, UNIPARC:UPI0000126582
C,Superfamily: H(+)-transporting ATP synthase gamma chain
C,Superfamily: H(+) biosynthesis; hydrolase; membrane-associated complex
A, Status: not compared with conceptual translation A; Molecule type: DNA
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Best Local Similarity
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A; Status: preliminary
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                                                                                                       "Jobate: 20-ppr.2004 #sequence revision 20-Apr.2001 #text_change 09-Jul-2004 C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Calobacter crescentus
C; Accession: C87425
E; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Froc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUD:21173698; PMID:11259647
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-378 <STO>
A; Residues: 1-378 <STO>
A; Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; FCGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
F, Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Redes: 1-173 <KUR>
A;Redes: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
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R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription. A;Reference number: S04666; MUID:85058188; PMID:6209404
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53;
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Pred. No. 7
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C;Superfamily: aldose 1-epimerase
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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282 NGPSGGAPR 290
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A; Status: preliminary
A; Molecule type: DNA
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A; Map position: II
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C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 1B-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Glass, J.I.; Leftowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min.
A;Reference number: A82870
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C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00378
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. S, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete A;Reference number: 214142; MUID:98403880; PMID:9734811
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M.Rebidues: 1-373 cGLAA,
A,Keebidues: 1-373 cGLAA,
A,Cross-references: UNIPARC:UP100000CLCAC, GB:AE002152; GB:AF222894; NID:g6899532; PIDN
A,Experimental source: serovar 3; biovar 1
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A,Molecule type: mRNA
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   DB 2;
   Score 41; DB
Pred. No. 81;
0; Mismatches
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A,Genetic code: SGC3
C,Superfamily: X-Pro aminopeptidase
   68.3%;
80.0%;
Query Match 68.3
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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A;Residues: 1-371 <WOO>
A;Cross-references: UNIPROT:O42905; UNIPARC:UPI00001352D5; EMBL:AL022117; PIDN:CAA17929
A;Experimental source: strain 972h-; cosmid c119
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: A86182
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nacure 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Li, J.H.; Lin, X.; Liu, X.; Liu, Z.X.; Liu, X.; Liu, X.; Liu, X.; Liu, Z.X.; Liu, X.; Liu, X.; Liu, Z.X.; Liu, Z.X.; Sinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Accession: A86181
A;Accession: A86182
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Modecule type: DNA
A;Residues: 1-383 <270>
A;Cross-references: UNIPROT:Q9MAT5; UNIPARC:UPI0000A6788; GB:AE005172; NID:g7211979; P
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                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39319
S;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
S;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
A;Wood, T.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
A;Wood, T.; Tansladted Library, March 1998
A;Accession: T39312
A;Accession: T39312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
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A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2
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Matches 7; Conservative
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7; Conserva
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Best Local S
Matches 7
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T36104
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                                                                   myristylated alanine-rich protein kinase C substrate - bovine
NyAlternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; $29270; A46098; PS0338
S;Stumpo, D.J.; Graff, J.M.; Albort, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinase
A;Reference number: S08341; MUID:89282412; PMID:2734111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: A32904
A, Status: nucleic acid sequence not shown
A, Status: nucleic acid sequence not shown
A, Status: nucleic acid sequence not shown
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-98, 'Q', 100-335 <ST2>
A, Cross-references: UNIPARC: UPI000017750A, GB: M24638; GB: M23738
A, Cross-references: UNIPARC: UPI000017750A, GB: M24638; GB: M23738
Bur. J. Biochem. 209, 7-14, 1992
A, Fletger, T.; Brocks, S.F.; Brocks, S.F.; Sroad, S.F.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P12624; UNIPARC:UP1000016C340; EMBL:M24638; NID:g163339; PID R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Netl. Acad. Sci. US.A. 86, 4012-4016, 1988
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-A;Reference number: A32904; MUID:89264553; PMID:2726763
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A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
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A; Molecule type: DNA
A; Residues: 191-253, 'SBE', 257-279, 283-292,'V', 294,'PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Residues: 191-253, 'SBE', 257-279, 283-292,'V', 294,'PEQE', 299,'A', 300,'A', 302-313,'A', 315
A; Cross-references: UNIPARC.UPI000017750B
B; Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
B; Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
A; Biol. Chem. 268, 6878-6881, 1993
A; Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A; Reference number: A46098; MUID:93216617; PMID:8463217
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A; Molecule type: protein
A; Residues: 2-11 - MAN.>
A; Residues: 2-11 - MAN.>
A; Cross-references: UNIPARC; UPI000017750C
R; Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A; Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with A; Reference number: PS0338; MUID:92171958; PMID:1540183
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A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UP1000017750D; UNIPARC:UP1000017750E; UNIPARC:UP1000017750F;
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C; Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
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Best Local Similarity 64...
Best Local Sy Conservative
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A; Residues: 1-335 <STU>
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C,Accession: T36104
R;Murphy, L:; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

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Gaps

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77.8%; Pred. No. 2.3e+02; ative 0; Mismatches 2;
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85.7%;
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
  Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                      173 AGGPGAGAP 181
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A;Molecule type: DNA
A;Residues: 1-103 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-954 <STO>
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A, Gene: APE0884
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A87431
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R; Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Rittle: Identification of a new class of steroid hormone receptors.

A; Reference number: A29345; MUID:88122546; PMID:3267207

A; Reference number: A29345; MUID:88122546; PMID:3267207

A; Residues: 1-521 «GIG>
A; Rosesion: A29345; MUID:88122546; PMID:3267207

A; Residues: 1-521 «GIG>
A; Roses references: UNIPROT:P11474; UNIPARC:UP10000142399; EMBL:X51416; NID:936608; PIDN

R; Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993

A; Title: SV40 early-to-late switch involves titration of cellular transcriptional repres

A; Reference number: A49074; MUID:94040741; PMID:8224847

A; Residues: 166-169, XX, 171-173 «WIL»

A; Cross-references: UNIPARC:UP1000017A1DF

C; Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi; 7;174-434/Demain: erbA transforming protein homology «ERBA»

F; 121-236/Region: zinc finger
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Species: Caulobacter createntus
Species: Caulobacter createntus
Species: Ol-Dec-1889 #sequence_revision Ol-Dec-1989 #text_change 09-Jul-2004
C.Accession: SO155
R.Accession: SO155
R.Accession: Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A.Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A.Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A.Refetence number: S02165
A.Accession: S02165
A.Accession: S02165
A.Molecule type: DNA
A.Residues: 1-679 < KAP>
A.Residues: 1-679 < KAP>
A.C.C.Genetics:
A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOED8:SCE15.01
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C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
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                                                                                                                                                          Score 40; DB 2; Length 436;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                          Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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465 AGPGGGAER 473
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S02165
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C, Accession: A87431
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy, A;Reference number: A72450; MUID:99310339; PMID:10382966
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72683
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ275978; CAB76945.1; -; mRNA.
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01-CCT-2002 (TrEMBLrel. 22, Last annotat
Hypothetical protein LAGE-2 (Fragment).
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Best Local Similarity
Local 11; Conservative
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q62H22 BURMA
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Q63HT9_BURPS
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Q4FKF7_9TRYP
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Q8NAC4 HUMAN
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                                                                                                                                                                                                                                                                                                                                         Figiter M.;
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galgoczy P., Platzer
Submitted (MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                               [5]
NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                  Platzer M
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      RRTTAR SERVICE SERVICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMID outstation the European Bloinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
-!- SIMILARITY: Belongs to the CTAG family.
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10-MAY-2005 (TrEWBLrel. 30, Last sequence update)
10-MAY-2005 (TrEWBLrel. 30, Last annotation update)
Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis antigen 1-A).
                                                                                                                   MEDIANE-19828962; PubMed=9626360; Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano de Plaen B., Boon T.; Landg-1, a new gene with tumor specificity."; Int. J. Cancer 76:903-908(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 100.0%; Score 60; DB 1; Length 180; Il Similarity 100.0%; Pred. No. 0.49; 11; Conservative 0; Mismatches 0: Indele
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Gly-rich.
; B122C5C2C8BE1569 CRC64;
   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
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EMBL; AJ003149; CARA65908.1; -; mRNA.
EMBL; AF038567; AAD05202.1; -; mRNA.
HGNC; HGNC:2491; CTAGIB.
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Matches 11; Conserv
                                                                                                     rissue=Melanoma;
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Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99454989; PubMed=10523621;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
De Smet C., Lurquin G., Lethe B., Martelange W., Boon T.;
Inne- and tumor-specific genes with a CpG-rich promoter.";
Mol. Cell. Biol. 19:7327-7335(1999).
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"Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes."; Hum. Mol. Genet. 10:2557-2567(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=993255C0; PubMed=10399963;
MEDLINE=99325SC0; PubMed=10399963;
Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
"Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
unexpected translation product of LAGE-1.";
Int. J. Cancer 82:442-448(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAG2 HUMAN STANDARD; PRT; 210 AA.
O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
Name=CTAG2; Synonyms=ESO2, LAGE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [7]
NUCLEOTIDE SEQUENCE.
Lethe B.G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           Platzer M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.;
to the EMBL/GenBank/DDBJ databases.
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B122C5C2C8BE1569 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF277315; AAL27014.1; ; Genomic_DNA.
EMBL; AJ27597; CABZ6643.1; -; Genomic_DNA.
EMBL, AF277315; AALZ7013.1; -; Genomic_DNA.
EMBL AF277315; AALZ7013.1; -; Genomic_DNA.
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TISSUE=Melanoma;
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us-09-529-206e-30.rup

1 RASGPGGGAPR 11

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WEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Latschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Batt N.K.,
HOKKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,
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Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQRPGTPGPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
QRR (in isoform LAGE-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mathtt{Pol}_{\mathbf{Y}}	extsf{-Pro} . MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPXHKV
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publicantive applicing; Named isoforms=2;
Name=LAGE-1B; Synonyms=LAGE-1L;
IsoId=075638-1; Sequence=Displayed;
Name=LAGE-1A; Synonyms=LAGE-1S;
Name=LAGE-1A; Synonyms=LAGE-1S;
IsoId=075638-2; Sequence=VSP_004301;
ISSUE SPECIFICITY: Testis and very low level in placenta and in some uterus samples. Observed in 25-50% of tumor samples of melanomas, non-small-cell lung carcinomas, bladder, prostate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Antigen; Polymorphism; Transmembrane.
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/FTId=VAR_007857.
8BB0EE000AE55E8BE_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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/FTId=VAR_007855.
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Pred. No. 8.3;
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EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
EMBL; AJ223040; CAA11043.1; -; mRNA.
EMBL; AJ223041; CAA11044.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSG0000126890; Homo sapiens.
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AJ012835; CAA10196.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   head and neck cancers.
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Best Local Similarity
Matches 10; Conserv
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STRAINENSDAYS)

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BURGALSTAT794; DOI=10.1073/pnas.0403302101;

A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,

Atkins T., Croseman L.C., Pitt T., Churcher C., Mungall K.L.,

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Burkholderia pseudomallei.";

Broc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

BRBL; BSK71965; CAHSG4661; -; Genomic DNA.

GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0002860; P:DNA poll3 delta.

R InterPro; IPR001272; DNA poll3 delta.

R InterPro; IPR0128; holA; 1.
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                                                                                                                                                                                                                            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
NCBI TaxID=28450;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DNA polymerses III, delta subunit (EC 2.7.7.7).

Name=holA; OrderedLocusNames=BMA2451;
Burkholderia anallei (Pseudomonas mallei).

Bacferia; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 23344;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 362;
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                                                                                                                                                                           Putative DNA polymerase III.
OrderedLocusNames=BPSL2936;
Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Pred. No. 28;
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                                                                                         PRT;
                                                                                053078 BURPS PRELIMINARY;
063078;
25-007-2004 (TrEMBLrel. 28, C.
25-007-2004 (TrEMBLrel. 28, Li
25-007-2004 (TrEMBLrel. 28, Li
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81.8%;
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   RASGPRGGAPR 62
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   STRAIN=K96243;
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   25
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157 RAKGGGGGAPR 167
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Peldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
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Zafar N., Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. US.A., 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
1-FBE-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein OJ1191_A10.131 (Hypothetical protein
OJ1014 E06.5).
Name=OJ1191_A10.131; Synonyms=OJ1014 E06.5;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0005260; F:DNA replication; IEA.
InterPro; IPR010372; DNA_pol3_delta.
InterPro; IPR005799; DNA_pol1II_delta.
Pfem; PF06444; DNA_pol3_delta.
IIGRFAMS; TIGR01128; holA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.3%; Score 47; DB 2; Length 449; llarity 81.8%; Pred. No. 94; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%; Score 50; DB 2; Length 362; 81.8%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-! SHILLARITY: Contains I RING-type zinc finger.
EMBL; AP0038857; BAD08744.1; -; Genomic DNA.
EMBL; AP003888; BAD11573.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Hypothetical protein; Metal binding; Zinc; Zinc-finger.
SEQUENCE 449 AA; 47196 MW; BBEFF7708B292296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
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Q7F1E3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 RAAGPGGDAPR 359
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                           BMA2451;
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       SOW WHEN THE PROPERTY OF THE P
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RASGPGGGAPR 11

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MEDLINE-97174314; PubMed-9022048; MCROTY J.B., Parker R.L., Sherwood N.M.; Expression and alternative processing of a chicken gene encoding both growth hormone-releasing hormone and pituitary adenylate cyclase-activating polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GHRH);
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2CP-C;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Anaeromyxobacter
debalogenans 2CP-C.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACA_CHICK STANDARD; PRT; 175 AA.

941534, 053WW0;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
11-JUL-1998 (Rel. 36, Last sequence released)
11-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (GH)
14-SEP-2005 (Rel. 48, Last annotation update)
15-SEP-2005 (Rel. 48, Last annotation update)
16-SEP-2005 (Rel. 48, Last annotation update)
16-SEP-2005 (Rel. 48, Last annotation update)
16-SEP-2005 (Rel. 48, Last annotation update)
17-SEP-2005 (Rel. 48, Last annotation update)
18-SEP-2005 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehalogenans 2CP-C.";
submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AAHD01000013; EAL79351.1; -; Genomic DNA.
SEQUENCE 895 AA; 93871 WW; 0AE25BBBF172BDB0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
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81.8%; Pred. No. 1.8e+02;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                    895 AA.
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                                                                                                                                             Created)
                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
QANUKA_9DELT PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=AdehDRAFT 2813;
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wes 9; Conserv
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TISSUS=Pancheas;

XX TISSUS=Pancheas;

XX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Atrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altschul S.P., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachay J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Multing M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15377794; DOI=10.1073/pnas.0403302101;
Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative lipoprotein.
OrderedLocusNames=BPSS2331;
Burkholderia pesudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Beraproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.7%; Score 46; DB 2; Length 194;
80.0%; Pred. No. 58;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Pancreas;
Director MGC Project;
Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015174; AAH15174.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Q63HT9;
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      Name=PLEKHG2;
Homo sapiens (Human).
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                                                                                                                                                   NCBI_TaxID=9606;
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                                                                               PRINTS; PRUUZIS; CLUCAGON; 2.
PROSITE; PSO0260; GLUCAGON; 2.
Alternative splicing; Amidation; Cleavage on pair of basic residues;
Direct protein sequencing; Glucagon family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pitultary adenylate cyclase activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pituitary adenylate cyclase activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone-releasing factor 1-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leucine amide (G-158 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group).
Lysine amide (G-169 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group).
RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG
(in isoform GRF 33-46).
/FTId=VSP_001759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1; Length 175; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODB54995FOAA9DFB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PLEKHG2 protein (Fragment).
                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3; Name=GRF 1-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P41534-3; Sequence=VSP 001759;
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=P41534-2; Sequence=VSP_001760;
Name=GRF 33-46;
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P41534-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U71183; AAB51200.1; -; mRNA.
ERME; U71184; AAB51201.1; -; mRNA.
EMBL; U71185; AAB51202.1; -; mRNA.
EMBL; U67275; AAC64494.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Cell Biol, 16:95-102(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000532; Glucagon.
Pfam; PF00123; Hormone 2; 2.
PRINTS; PR00275; GLUCAGON.
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                                                    PROTEIN SEQUENCE OF 131-168.
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Q96BUZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.
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                                                                                                                                                                                                                                                                                                                                                                                                            Name=GRF 1-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
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Chromosome undetermined SCAF5395, whole genome shotgun sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUDMEd=1537793; DOI=10.1073/pnas.0403306101; Nelson K.E., PubMed=1537793; DOI=10.1073/pnas.0403306101; Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Nelson T.U., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M.; "Structural flexibility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitchead S., Yaats C., Barrell B.G., Oyston P.C.F., Parkhill J.; "Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei."; Burkholderia pseudomallei."; EMBL; BX511966; CAH39817.1; -; Genomic_DNA.

GO, GO:0016020; C:membrane; IEA.

InterPro; IPR007428; VacJ.
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0
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Burkholderiaceae, Burkholderia.
NCBI_TaxID=13373;
                                                                                                                                                                                                                                                                                    76.7%; Score 46; DB 2; Length 327;
88.9%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.7%; Score 46; DB 2; Length 330; 88.9%; Pred. No. 97; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                    Complete proteome; Lipoprotein.
SEQUENCE 327 AA; 33687 MW; AC5D2C7CC4A44A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Lipoprotein.
SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative lipoprofesin.
OrderedLocusNames=BMAA2092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
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                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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nterPro; IPR007428; VacJ.
fam; PF04333; VacJ; 1.
                                                                                                                                                                           Pfam; PF04333; VacJ; 1.
PRINTS; PR01805; VACJLIPOPROT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01805; VACJLIPOPROT
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Q4TEG9;
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                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     243 AGGPGGGAP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AGGPGGGAP 251
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Best Local Similarity
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13-SEP-2005
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Q4TEG9_TET
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micale D., Fisher S., Luffalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Botak S., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., Wichney B., Lander E.S., Weissenbach J., Roest Crollius H., McGnomel duplication in the teleost fish Tetraodon nigroviridis reveals
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Bukaryota, Pungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes;
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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PubMed=15653466; DOI=10.1126/science.1103773;
Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
                                Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Edinopterygii, Neopterygii, Teleostei, Butaleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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Van Aken S., Fraser C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope; Whitehead Institute Centre for Genome Research, Submitted (FBS-2004) to the EMBL/GenEank/DBBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.7%; Score 46; DB 2; Length 383
80.0%; Pred. No. 1.18+02;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA; 39582 MW; A61F4ECF2EEC3861 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MXY-2005 (TrEMBLrel. 30, Created)
10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Actin Cross-linking, putative.
ORFNames=CNC06000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAE01005395; CAF88713.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
ORFNames=GSTENG00002257001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRYNE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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NUCLEOTIDE SEQUENCE.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=214684;
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"Cryptococcus moeformans serocype D sequencing.";

Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an BMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAEY01000013; EAL21978.1; -; Genomic_DNA.

REMBL; AAEY0100013; EAL21978.1; -; Genomic_DNA.

RO; GO; 0005509; F: calcium ion binding; IEA.

InterPro; IPR00115; Calpoin_nact_bd.

InterPro; IPR00115; Calpoin_nact_bd.

RITERPO; IPR001192; EF-Hand type.

RITERPO; IPR001017; Spectrin.

REMBL; PS00019; ACTININ 1; UNKNOWN 1.

REMSTE; PS00019; ACTININ 2; UNKNOWN 1.

REMSTE; PS00012; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCB1_TaxID=283643;
Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.K., Salzberg S.L., Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Wye N.H., Kronstad J.W., Lodge J.K., Mickes B.L., Wortman J.R., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., "The genome of the basidiomycetous yeast and human pathogen Cryptococcus neoformans.";
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Science 307:131-1324 (2005).

REMBL; AE017343; AAW42672.1; -; Genomic_DNA.

GO; GO:0003709; F:actin blinding; IEA.

GO; GO:0005509; F:actin blinding; IEA.

InterPro; IPR001589; Actnin actin_bd.

InterPro; IPR001515; Calponin act_bd.

InterPro; IPR002017; Spectrin.

Refan; PF00307; CH; 2.

RAMART; SW00019; ACTININ_1; UNKNOWN_1.

RESOSITE; PS00019; ACTININ_2; 1.

REOSITE; PS00020; ACTININ_2; 1.

REOSITE; PS00020; ACTININ_2; 1.

REOSITE; PS00020; ACTININ_2; 1.

RECOMPLETE PROFESSION ACTININ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.7%; Score 46; DB 2; Length 708; 88.9%; Pred. No. 2.18+02; ative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptococcus neoformans var. neoformans B-3501A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, 613-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 14) Hypothetical protein. ORFNames=CNBC1180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CRYNE
Q55WM1 CRYNE PRELIMINARY;
Q55WM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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STRAIN=B-3501A;
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SEQUENCE 708 AA;
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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0558M1 CRY
DD 7558M
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AC 0558M
DD 13-SE
DT 13-SE

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps QY 2 ASGPGGGAP 10

Db 47 AGGPGGAP 55

Search completed: March 13, 2006, 19:14:29
Job time: 80.8471 secs
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Sequence 19986, A Sequence 562, Appli Sequence 6, Appli Sequence 43766, A Sequence 43766, A Sequence 17549, A Sequence 27111, A Sequence 31361, A Sequence 376, Appl Sequence 17549, A Sequence 17549, A Sequence 17549, A Sequence 176, Appl Sequence 176, Appl Sequence 11, A Sequence 276, Appl Sequence 19543, A Sequence 20489, A Sequence 20489, A Sequence 20489, A Sequence 20489, A Sequence 10543, A Sequence

18782, A 19986, A 562, Appli 6, Appli 6, Appli 33219, A 3369, Ap 17549, A 3299, A 3299, A

Sequence:

Run on:

Searched:

Database

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Result

46978601221111111122222222

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100.0%; Score 60; DB 1; Length 180; 100.0%; Pred. No. 0.69; cive 0; Mismatches 0; Indels
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ZIP: 02210
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHIN RC-BOS/NS-DOS
SOFTWARE: PATCHIN NUMBER: US/08/791,495
ATCORNEY/AGENT INFORMATION:
NAME: VAN AMSTECTAM JOHN R.
REGISTRATION NUMBER: 40,212
REDERMICH/DOCKET NUMBER: 10461/7005
TELEPRAN: 617-720-3500
TELEPRAN: GATO SOTO NOTO.
                     US-09-252-991A-19986
US-08-949-002-562
US-08-949-002-562
US-08-91A-30219
US-09-272-796-6
US-09-272-796-6
US-09-272-91A-30219
US-09-252-991A-32992
US-09-252-991A-30361
US-08-976-255-1
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US-09-252-991A-20489
US-09-902-540-12423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTYON: LL-1 TUMOR SPECIFIC GENES
CORRESPONDENCE: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08791495; Patent No. 5811519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: IENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 11, Conservative
                        310
340
412
412
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416
553
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807
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US-08-791-495-9
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Sequence 8, Appli
Sequence 25, Appli
Sequence 15, Appli
Sequence 30, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 117, Appli
Sequence 3, Appli
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Sequence 21, Appl
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                                                                                                                                                                                                      (without alignments)
44.477 Million cell updates/sec
                                                                                                                                                                      March 13, 2006, 19:14:49 ; Search time 20.4471 Seconds
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                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-372-263B-8
US-09-392-714-25
US-09-316-546D-15
US-09-341-829A-9
US-09-341-829A-9
US-09-341-829A-7
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US-09-341-829A-7
US-09-341-829A-7
US-09-321-829A-7
US-09-252-991A-77249
US-08-252-991A-77249
US-08-252-991A-77249
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US-09-252-991A-17831
US-09-491-356C-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                               Sequence 8, Application US/08937263B
Sequence 8, Application US/08937263B
Sequence 8, Application US/08937263B
Sequence 8, Application US/08937263B
Setent No. 6274145
GENERAL INFORMATION:
APPLICANT: Gure, Ali Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifthout. An W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ITSELF, AND USES THEREOF
INVENTION: ITSELF, AND USES THEREOF
STREET: 666 Fifth Avenue
CITT: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
COMP
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APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Chen, Yao-tseng; Scanlan, Liber, Lancer TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 cancer TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA TITLE OF INVENTION: Binding Peptides Derived Therefrom NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gibright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITT: New York City
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CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/72,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SIN, ERIC, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEG ID NO: 8:
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100.0%; Pred. No. 0.69;
tive 0; Mismatches 0; Indels
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US-09-392-714-25

Sequence 25, Application US/09392714A

Patent No. 6686147

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Glure, Ali O.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Llow Glure, Ali
APPLICANT: 1046,17062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
ERALIER PILING DATE: 1998-09-05

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NOS: 30

SEQ ID NOS: 30

SEQ ID NOS: 30
COUNTY: 10103
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: OCTOBER 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HARBON, NO. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5466.
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.v.
These 11; Conservative
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ORGANISM: Homo sapiens
US-09-392-714-25
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TOPOLOGY: linear
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Best Local Similarity
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    <151> 1998-01-27
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Pred. No. 0.69;
; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Scanlan, Matthew J.
APPLICANT: Scanlan, Matthew J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105(JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucias, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Fallen, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
PRIOR APPLICATION NUMBER: PCT/US98/01445
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 30, Application US/09849602; Patent No. 6794501; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/08791495; Patent No. 5811519
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100.0%; Some Best Local Similarity 100.0%; P. Matches 11; Conservative 0;
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MEDIUM TYPE: Floppy
                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conserv
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LENGTH: 180
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US-08-791-495-7
                                                                    SEQ ID NO 9
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                                                                                                        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
COMPUTER: IBM
COPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: APPLICATION NUMBER: 09/062,422
FILING DATE: September 15, 1997
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY AGENT INFORMATION:
NAME: Hanson, NO. 6729332man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 2166.4 CIP (09807811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <151> 1997-01-27
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APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LAGS-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: Lo461/7066
CURRENT APPLICATION NUMBER: US/09/341,829A
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 08/791,495 <151> 1997-0
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                        Sequence 15, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09341829A
Patent No. 6794131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 180 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 318-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                CITY: New York City
STATE: New York
                                                                                                                                                                                                                          SZQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match , 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                          NUMBER OF
                   US-09-165-546D-15
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<151> 1997-01-27 <151> 1998-01-27
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Pred. No. 8.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%; Score 52; DB 1; Length 210; 90.9%; Pred. No. 8.6; ive 0; Mismatches 1; Indels
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
E: Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                            L0461/7005
                                                                                                                                                                                                                                      APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amseerdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0467
TELECOMMUNICATION INFORMATION:
TEPPONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09341829A Patent No. 6794131
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                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617-720-3500
TELEPAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 210 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-791-495-5
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US-09-341-829A-5
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Best Local Similarity
Matches 10; Conserv
                                                                            USA
                                                                          COUNTRY: US
ZIP: 02210
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7. Application US/09341829A
Patent No. 6794131
GENERAL INPORMATION:
APPLICANT: Leth., Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Goon-Falleur, Thierry
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
FILE REFERENCE: L0461/7066
CURRENT FILING DATE: 1999-10-18
FRIOR APPLICATION NUMBER: US 08/791,495
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRESENCE for Windows Version 3.0
SEQ ID NO 7
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 1; Length 180;
Pred. No. 7.5;
0; Mismatches 1; Indels
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Patent No. 5011519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smer, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
            FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFRENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-341
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-791-495-7
APPLICATION NUMBER: US/08/791,495
                                                                                                                                                                                                                                                                                                                                                          Query Match '86.7%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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US-08-791-495-5
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Gaps

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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31759
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: SHERWOOD ET AL.
TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL.
TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Whinston, Lip
STREET: 121 S.W. Salmon Street
STREET: 121 S.W. Salmon Street
STREET: 121 S.W. Salmon Street
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: 121 S.W. Salmon Street
STREET: Disk Walte 1600
CITY: Portland
STREET: Oregon
COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
PILING DATE: 01/23/97
CLASSIFICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 2;
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Barp, David J.
REGISTRATION NUMBER: 41,401
REFREENCE/POCKET NUMBER: 2847-46468/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8
Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 RAGGPRGGAPR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RASGPGGGAPR 11
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Sequence 117, Application US/09344040C

Sequence 117, Application US/09344040C

Batent No. 6548064

GENERAL INFORMATION:

APPLICANT: Tureci, Ozlem

APPLICANT: Ramensee, Hand Georg

APPLICANT: Ramensee, Hand Georg

APPLICANT: Ramensee, Hand Georg

TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin

TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

TITLE OF INVENTION: Gene, and Uses Thereof

FILE REFERENCE: LUD 5556.1

CURRENT APPLICATION NUMBER: US/09/344,040C

CURRENT PILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

PRIOR FILING DATE: 1999-06-26

NUMBER OF SEQ ID NOS: 132

SEQ ID NO 117

LENGTH. 0
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Batent No. 6673350

GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT FILING DATE: 1099-06.25
PRIOR PILING DATE: 1999-06-25
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1999-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
NUMBER OF FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 131
SOUTHARE PLENTIN Version 3.2
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US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
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Best Local Similarity 100...
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Best Local Similarity 100...
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-833-039A-117
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ORGANISM:
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                                    0; Gaps
Query Match 76.7%; Score 46; DB 2; Length 143; Best Local Similarity 72.7%; Pred. No. 36; Matches 8; Conservative 0; Mismatches 3; Indels
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¹ RASGPGGGAPR 11 || || || || || 56 RAGAPGGGGPR 66

Search completed: March 13, 2006, 19:18:52 Job time: 20.4471 secs

1436, Ap 388, Ap 388, App 141, App 69, App 75, App 175, App 75, App 77, App

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 76, Appl Sequence 5, Appli

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 1404, Application US/10296734

| Publication No. US20040054137A1
| Publication No. US20040054137A1
| GENERAL INFORMATION:
| APPLICANT: Thompson, Scott A
| TITLE OF INVENTION: Synthetic molecules and uses therefor TITLE REFERENCE: Savine 2003.08-04
| CURRENT FILING DATE: 2003.08-04
| PRIOR PILICATION NUMBER: US/10/296,734
| CURRENT FILING DATE: 2000-05-26
| NUMBER OF SEQ ID NOS: 1507
| SOFTWARE: Patentin version 3.2
| LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 60; DB 4; Length 30; Similarity 100.0%; Pred. No. 0.48; 11; Conservative 0; Mismatches 0; Indels
US-10-447-161-39

US-10-415-841A-52

US-10-182-506A-23

US-10-296-734-1436

US-10-295-027-388

US-10-188-8132-141

US-10-117-937-75

US-10-10-734-834

US-10-657-022-75

US-10-657-022-75

US-11-067-169-75

US-11-067-169-75

US-11-067-169-75

US-11-067-169-75

US-11-17-937-76

US-11-17-937-76

US-10-157-031-88

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US-10-157-031-88
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US-10-296-734-1404
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US-10-482-029-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 11; Conserv
    991.7
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      TYPE: PRT
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Sequence 1270, Ap
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 5024, Ap
Sequence 74, Appl
Sequence 74, Appl
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Sequence 27, Appl
Sequence 1454, Ap
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Sequence 30, App
                                                                                                                                   March 13, 2006, 19:51:56 ; Search time 66.5176 Seconds (without alignments) 69.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3
Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-067-064-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-296-734-1454
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US-10-182-506A-3
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                                                                                                 - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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60
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Maximum DB seq length: 2000000000
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Patent No. US20020010321A1

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.

TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1

TITLE OF INVENTION: Associated Proteins, UBes Thereof,
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES:
8
    100.0%; Score 60; DB 5; Length 179; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 60; DB 3; Length 180; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1966
AFTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321Alman D.
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                              1 RASGPGGGAPR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-849-602-30
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Publication No. US20020164665A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer;
Handled Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 60; DB 3; Length 180; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, No. US20020164665Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
                 APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: COLON Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: CUBKNOWN
APPLICATION NUMBER: 08/725,182
FILING DATE: OCCOBER 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
Stockert, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 752-:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
warches 11; Conservative
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                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens US-09-849-602-30
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Gaps
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                          APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: BRITOPE SYNCHRONIZATION IN ANTIGEN
TITLE OF INVENTION: PRESENTING CELLS
FILE REFERENCE: CTLIMM.21CPIC
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT PILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PRILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PRILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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100.0%; Score 60; DB 4
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches
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Publication No. US20030220239A1
GENERAL INPORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
TITLE NOF INVENTION: BETTOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
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ORGANISM: Homo sapiens
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US-10-117-937-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-026-066-3
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Sequence 14, Application US/10364614

Sequence 14, Application US/2030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: Glatic, Sacha

TILLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-34

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR APPLICATION NUMBER: US 60/355,828

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.2
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                                                                   Gaps
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Publication No. US20030118592A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-4011.
CURRENT APPLICANTON NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 60; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 11; Conservative 0; Mismatches 0; Indels
  100.0%; Score 60; DB 4; Length 180; 100.0%; Pred. No. 2.3;
                                                           0; Indels
                                                           0; Mismatches
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US-10-026-066-3
Sequence 3, Application US/10026066
; Publication No. US20030215425A1
Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                   1 RASGPGGGAPR 11
                                                                                                                                                      1 RASGPGGGAPR 11
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US-10-207-655-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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LENGTH: 180
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LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Matray, Richard H.
APPLICANT: Matray, Richard H.
APPLICANT: Mateon, Susan R.
APPLICANT: Mateon, Susan R.
APPLICANT: Mateon, Susan R.
APPLICANT: Mateon, Susan R.
APPLICANT: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US/00-09-15
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR PILING DATE: 2000-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-11-21
PRIOR PPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-21
PRIOR PPLICATION NUMBER: US 60/347,211
PRIOR PPLICATION NUMBER: US 60/347,211
PRIOR PPLING DATE: 2001-12-14
PRIOR PPLING DATE: 2001-12-14
PRIOR PPLING DATE: 2001-12-14
PRIOR PPLING DATE: 2002-01-06
PRIOR PLING DATE: 200
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Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine

CURRENT APPLICATION WUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR PILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: PALENTIN NOS: 1507
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                         Sequence 386, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                       Glynne, Richard
Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                             Mack, David H.
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserva
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US-10-296-734-832
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RESULT 13
US-10-777-053-11
is Sequence 11. Application US/1077053
is Publication No. US20040132088A1
is GENERAL INFORMATION:
is APPLICANT: Simard, John J. L.
is APPLICANT: Qiu, Zhiyong
is APPLICANT: Qiu, Zhiyong
is APPLICANT: Lei, Xiang-Dong
is TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
it TITLE OF INVENTION: ADMURER: US/10/777,053
is CURRENT APPLICATION NUMBER: US/10/777,053
is CURRENT FILING DATE: 2004-02-10
is PRIOR PILING DATE: 2002-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us-10-180-03-4-13)

Sequence 139, Application US/10188832

Publication No. US20040076955A1

Sequence 139, Application No. US20040076955A1

SERBERAL INFORMATION:
APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Ese Biotechnology, Inc.
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

CURRENT APPLICATION NUMBER: US/10/188,832

CURRENT APPLICATION NUMBER: US 60/302,814

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-07-03

PRIOR PELING DATE: 2001-08-03

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 207

NUMBER OF SEQ ID NOS: 207
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                                                                 ; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Artificial
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Gaps
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                                                                                                                                          US-10-657-022-74

| US-10-657-022-74
| Sequence 72, Application US/10657022
| Publication No. US20040180354A1
| GENERAL INPORMATION:
| APPLICANT: Simard, John J. L.
| APPLICANT: Diamond, David C.
| APPLICANT: Liu, Liping
| TITLE OF INVENTION: EPITOPE SEQUENCES
| TITLE OF INVENTION: EPITOPE SEQUENCES
| CURRENT APPLICATION NUMBER: US/10/657,022
| CURRENT FILING DATE: 2003-09-04
| PRIOR APPLICATION NUMBER: 60/409123
| PRIOR APPLICATION NUMBER: 60/409123
| PRIOR APPLICATION NUMBER: 00/409123
| SOFTWARE: FASESQ for Windows Version 4.0
| SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 60; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                     1 RASGPGGGAPR 11
                                                                             52 RASGPGGGAPR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Gure, Ali, Old, Lloyd, Ritter, Gerd
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
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COMPUTER READABLE FORM:

COMPUTER: 1BM
COMPUTER: 1BM
COMPUTER: 1BM
COPRATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFTCATION DATA:
FILING DATE: 02-Jan-2004
FRIOW APPLICATION DATA:
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100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                DB 4; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811) TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICK AFFLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                            Query Match 100.0%; Score 60; DB 4 Best Local Similarity 100.0%; Pred. No. 2.3; Matches 11; Conservative 0; Mismatches
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SEQ ID NO 11
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: HOMO Sapien
US-10-777-053-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, Norman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-751.088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 180 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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March 13, 2006, 19:54:06; Search time 7.50588 Seconds (without alignments) 40.793 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USON_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USON_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USI1_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits; satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             161667 segs, 27834885 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                     US-09-529-206E-30
60
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                        1 RASGPGGGAPR 11
                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ş		7, Appli	28, Appl	496, App	3295, Ap						66, Appl		262		7762		58,	223			22332, A	8	2	54, Appl	18, Appl	63, Appl
Dogorithic	הפפנדוקרדו	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
Ę		US-11-155-288-7	US-11-021-441-28	US-10-623-155-496	US-11-072-512-3295	US-11-096-568A-20556	US-11-096-568A-23806	US-11-108-528-58	US-11-179-958A-2	US-11-072-512-3369	US-11-037-243-66	US-11-143-980-34	US-11-096-568A-26217	US-10-531-036-35	US-11-087-099-7762	US-11-072-512-2722	US-11-240-769-58	US-11-096-568A-22334	US-11-096-568A-22333	US-11-096-568A-27265	US-11-096-568A-22332	US-10-992-577-8	US-10-508-892-2	US-11-223-294-54	US-11-078-735-18	US-11-050-346-63
ä	3	7	7	y	7	7	7	7	7	7	7	7	7	9	7	7	7	7	7	7	7	9	9	7	7	7
tono.		180	240	20	678	306	134	365	537	555	953	280	558	974	1832	213	233	353	358	413	420	430	430	430	618	618
% Ouery Match		100.0	100.0	80.0	75.0	71.7	70.0	68.3	68.3	68.3	68.3	67.5	4.99	66.7	66.7	65.0	65.0	65.0	65.0	65.0	65.0	65.0	65.0	65.0	65.0	65.0
2	3000	9	9	48	45	43	42	41	41	41	41	40.5	40	40	40	39	39	39	39	39	39	39	39	39	39	39
Result	2	1	73	n	4	S	9	7	œ	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 18, Appl Sequence 1843, App Sequence 1843, A Sequence 2845, A Sequence 22603, A Sequence 22603, A Sequence 12071, A Sequence 188, Appl Sequence 2187, A Sequence 2187, A Sequence 342, Appl Sequence 342, Appl Sequence 11165, A Sequence 128, Appl Sequence 342, Appl Sequence 22494, A Sequence 22494, A	Seguence 11283, A Seguence 24377, A Seguence 16, Appl
US-11-103-077-18 US-11-096-568A-14323 US-11-096-568A-14323 US-11-096-568A-22845 US-11-096-568A-22845 US-11-096-568A-22071 US-11-096-568A-22071 US-11-096-568A-988 US-11-096-568A-988 US-11-096-568A-988 US-11-087-099-9800 US-11-087-099-11165 US-11-096-568A-10542 US-11-096-568A-10542 US-11-096-568A-10542 US-11-096-568A-10542 US-11-096-568A-10542 US-11-096-568A-10542 US-11-096-568A-10542	US-11-096-568A-11283 US-11-096-568A-24377 US-11-109-156-16
LLLLLLL017777	7
618 6628 1322 2368 2368 3306 44330 11219 11219 11219 11219 11219 11219 11219 11219	328 375 379
65.0 633.3.3.3.3.3.6 633.3.3.3.6 611.7.7 611.7.7 611.7.7	61.7 61.7 61.7
	37 37
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## ALIGNMENTS

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Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DUCKETY, William S., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF
FILE REPERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT APPLICATION NUMBER: US 60/616,750
PRIOR APPLICATION NUMBER: US 60/616,750
                                                                                             APPLICANT: Chiang, Chih-Sheng
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANITORNS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANNK. 050A
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FRRESEQ FOR WINDOWS Version 4.0
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                   ; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RASGPGGGAPR 11
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US-11-155-288-7
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US-11-021-441-28
US-11-155-288-7
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US-11-096-568A-20556

Sequence 20556, Application US/11096568A

Sequence 20556, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23806, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 7; Length 678; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.7%; Score 43; DB 7; Length 306; 80.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | NAME/KEY: misc_feature
| LOCATION: (1)...(306)
| OTHER INDEMATION: Ceres Seq. ID no. 12383286
| US-11-096-568A-20556
                                                                                            APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SOSHIKAWA, TSUTOMU
APPLICANT: OYSHIKAWA, TSUTOMU
APPLICANT: OYSHIKAWA, MOTOVUKI
APPLICANT: MASUHO, YASUHIKO
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTION OF 11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 3295
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Best Local Similarity 80.0°
Local 8; Conservative
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Best Local Similarity 80.v.
8, Conservative
                                                     NAGAI, KEIICHI
IRIE, RYOTARO
                               OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 RÁAGPGGGWP 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-072-512-3295
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Sequence 496, Application US/10623155

Publication No. US20050261166A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Rettef, Marc W.

APPLICANT: Rettef, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C20

CURRENT APPLICATION NUMBER: US/10/623,155

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 60; DB 7; Length 240; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 11; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PSESSEQ for Windows Version 4.0
SSOFTWARE: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 48; DB 100.0%; Pred. No. 0.6 tive 0; Mismatches
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US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
; APPLICANT: GUINTAMA, TOMOYASU
; APPLICANT: GUINTAMA, TOMOYASU
; APPLICANT: MAXAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: ISHOO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Fusion protein US-11-021-441-28
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.0
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 RASGPGGGAPR 122
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JS-10-623-155-496
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                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.3%; Score 41; DB 7; Length 555; 77.8%; Pred. No. 88; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASTHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT PILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: UP 2001-379298
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR SELING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
                    PRIOR APPLICATION NUMBER: 60/586,909
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
ENGTH: 537
                                                                                                                                                                                                     FEATURE:
, OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3369, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XESULT 10
US-11-037-243-66
; Sequence 66, Application US/11037243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SIGGAL, TAKAO
APPLICANT: SIGGIANA, TOMOYASU
APPLICANT: CUSUKI, TERSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: STO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, UUN-ICHI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                          68.3%;
70.0%;
                                                                                                                                                                                                                                                                                        Query Match 68.3
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                    1 RASGPGGGAP 10
                                                                                                                                                                                                                                                                                                                                                                                                                    36 RSPGPGAGAP 45
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                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-072-512-3369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ASGPGGGAP 10
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Mary, Elizabeth
APPLICANT: Shamah, Elizabeth
APPLICANT: Shamah, Steven M.
ITILE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
ITILE OF INVENTION: MUMBER: US/11/108,528
CURRENT APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 365
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Publication No. US20060030537A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hannun, Yusef A.
APPLICANT: Pettus, Benjamin J.
APPLICANT: Bielawska, Alicja
TITLE OF INVENTION: Ceramide Kinase and Uses Thereof
FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
CURRENT APPLICATION NUMBER: US/11/179,958A
                                                                                                                                                                                                                     NAME/KEY: misc_feature
i_LOCATION: (1)..(134)
i_LOCATION: (1)..(134)
i_LOFIER INDEMATION: Geres Seq. ID no. 12415289
US-11-096-568A-23806
             FILE REFERENCE: 2750-1592PUSZ
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 23806
LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/11108528 Publication No. US20050261189A1 GENERAL INFORMATION:
                                                                                                                                                       TYPE: PRT ORGANISM: Zea mays subsp. mays
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                 Query Match 70.0
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Mouse US-11-108-528-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-108-528-58
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US-11-096-568A-26217
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APPLICANT: He, Fig. 1900

APPLICANT: Halti, Bradley A. APPLICANT: Halti, Bradley A. APPLICANT: Wagenar, Malissa M. APPLICANT: Graziani, Edmund APPLICANT: Summers, Mis APPLICANT: Summers, Mis APPLICANT: Summers, Mis APPLICANT: Rilowskii, Kerry APPLICANT: Pong, Kevin Northetic Gene Cluster for the Production of a Complex TITLE OF INVENTION: Bolyketide

TITLE OF INVENTION: Bolyketide

TITLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

TILLE OF INVENTION: Polyketide

TITLE OF INVENTION: Polyketide

TILLE OF INVENTION: Polyketide

TILLE OF INVENTION: Polyketide

FILE REFERENCE: AM-10142608

CURRENT APPLICATION NUMBER: US 60/664,483

PRIOR APPLICATION NUMBER: US 60/576,895

PRIOR FILING DATE: 2004-06-03

PRIOR FILING DATE: 2004-06-03

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn version 3.3

SEQ ID NO 34

LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.3%; Score 41; DB 7; Length 953; 87.5%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-56
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR PILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver: 2.1
SERVING 1D NO 56
LENGTH: 953
              GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CARNEPEEL, SAND
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERAED
APPLICANT: SUDARSANAM, SUCHA
TILE OF INVERTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/11143980 Publication No. US20050272133A1 GENERAL INFORMATION:
APPLICANT: He, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.5%;
75.0%;
Publication No. US20050287546Al
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Best Local Similarity 75.0
Matches 9; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 GPGGGHPR 221
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US-11-143-980-34
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RESULT 12

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Sequence 26217, Application US/11096568A

Publication No. US20060048240A1

Publication No. US20060048240A1

Publication No. US20060048240A1

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592E032

CURRENT APPLICATION NUMBER: US/11/096,568A

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 26217

LENGTH: 558
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APPLICANT: Eulenberg, Karsten
APPLICANT: Eulenberg, Martin
APPLICANT: Eulenberg, Martin
APPLICANT: Molitor, Andreas
APPLICANT: Molitor, Andreas
APPLICANT: Steuernagel, Arnd
ITILE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
FILE REFERENCE: 2923-696
CURRENT APPLICATION NUMBER: US/10/531,036
CURRENT FILING DATE: 2003-10-14
FRIOR PILING DATE: 2003-10-14
FRIOR PLILING DATE: 2002-11-06
FRIOR APPLICATION NUMBER: EP 02024747.4
FRIOR PILING DATE: 2002-10-22
FRIOR PLILING DATE: 2002-10-22
FRIOR PLILING DATE: 2002-10-14
FRIOR FILING DATE: 2002-10-14
FRIOR FILING DATE: 2002-10-14
FRIOR FILING DATE: 2002-10-14
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FRIOR FILING DATE: 2003-3
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Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 4;
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NAME/KEY: misc_feature

LOCATION: (1)._(558)

LOTTER INFORMATION: Ceres Seq. ID no. 13498878

US-11-096-568A-26217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-531-036-35
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US-11-087-099-7762
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Best Local Similarity 77.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION WUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7762
IENGTH: 1832
TYPE: PRT
ORGANISM: Podospora anserina
US-11-087-099-7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SUGIYANA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: YAMAMOYO, UNN-ICHI
APPLICANT: YAMAMOYO, UNN-ICHI
APPLICANT: TAMAGHAK, ICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TOSUKA, MODIVUKI
APPLICANT: TOSUKA, WODILIU
APPLICANT: OTSUKA, WODILIU
APPLICANT: OTSUKA, WODILIU
APPLICANT: OTSUKA, WONOYUKI
APPLICANT: NOBAHARI, KENJI
APPLICANT: NOBAHARI, KENJI
APPLICANT: NOBAHARI, KENJI
APPLICANT: NOBAHARI, KENJI
APPLICANT: NASUHO, YASCHIKAO
ITILE OF INVENTION: NOWBER: US/11/072,512
CURRENT FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER: PAEENLIN VOR: 2.1
SEQ ID NO 2722
LENGTHARE: PAEENLIN VOR: 2.1
LENGTHARE
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Job time : 7.50588 secs
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ORGANISM: Homo sapiens
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56 SGPGGGA 62
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US-11-072-512-2722
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